U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office **SEARCH REQUEST FORM** Attitude Delly Requestor's 68/938,548 Number: Art Unit: \_\_\_ Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s). Fleuse include an interference search. Thanks Pat STAFF USE ONLY Vendors Search Site STIC \_ CM-1 STN Terminal time: Pre-S Dialog Elapsed time: APS Type of Search CPU time: N.A. Sequence Geninfo SDC A.A. Sequence Number of Searches: DARC/Questel Structure Number of Datagases: Other

Bibliographic

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protein - protein database search, using Smith-Waterman algorithm

MasPar time 12.09 Seconds 591.342 Million cell updates/sec Fri Aug 20 20:53:06 1999; Run on:

MPsrch\_pp

Tabular output not generated.

>US-08-938-548B-2 (1-131) from US08938548B.pep 931

Description: Pèrfect Score:

1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_bhage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 39.956; Variance 91.033; scale 0.439 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score Match Length DB ID   Description	Pred. No.	1.03e-143	5.14e-128	1.46e-116	2.72e-115	2.1	1.60e-01	2.81e-01	3.71e-01	1.12e+00	1.12e+00	1.12e+00	1.47e+00	1.47e+00	1.93e+00	1.93e+00	2.52e+00	3.29e+00	4.29e+00	5.58e+00	5.58e+00
Ouery Score Match Length DB 845 90.8 131 4 845 90.8 131 6 775 84.0 130 11 110 11.8 132 14 100 10.7 480 4 100 10.7 480 4 96 10.3 400 4 96 10.3 453 10 95 10.2 256 2 95 10.2 382 2 95 10.2 1337 4 94 10.1 1337 4 94 10.1 1337 4 94 10.1 1337 4 94 10.1 1337 4 99 99 99 833 4 90 97 147 11	Description	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	PREPRO-OREXIN.	HYPOCRETIN (PREPRO-ORE	KIAA0634 PROTEIN (FRAG	HYPOTHETICAL 74.6 KD P	BAI 1.	POLYADENYLATE BINDING	NISHED (FRAGMENT).	GDNF FAMILY RECEPTOR A	MYB-LIKE DNA-BINDING D			PROTEIN-TYROSINE PHOSP	KIAA0612 PROTEIN (FRAG	ORF469 PROTEIN.	SORTILIN PRECURSOR.	MRNA ENCODING RAMP2 PR	3' ORF.	ACYLOXYACYL HYDROLASE.
200re 941 782 775 775 775 775 775 775 775 775 775 77	QI	043612	077668	055232	055241	075129	023352	014514	060455	042394	609090	049019	006319	087918	015255	075111	037839	099523	060895	061639	035298
200re 941 782 775 775 775 775 775 775 775 775 775 77	DB	4	9	11	11	4	10	4	4	13	4	10	7	7	4	4	σ	4	4	11	11
200re 941 782 775 775 775 775 775 775 775 775 775 77	Length	131	131	130	130	1321	619	1584	480	205	400	453	226	382	1337	1736	469	833	175	147	574
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131 AA.

PRT;

PRELIMINARY;

RESULT 2 ID 077668 AC 077668;

121 ASVAPGGOSGI 131 ||||||||||||||| 121 ASVAPGGOSGI 131

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R32184_2. LEUCINE-RICH REPEAT/RE 5 LEUCINE-RICH REPEAT/RE 5 FIL3 LIGAND, T169 FORM 7 NOVEL SERINE PROTESE. PHENOLOXIDASE (EC 1.10 9 PHENOLOXIDASE (EC 1.10 9 TIGHT JUNCTION PROTEIN 9 ANION EXCHANGER ISOFOR 1 ANION EXCHANGER 2 A (F 1 RIGOSOME RECEPTOR. MAVZ66 (FRAGMENT). HYPOTHETICAL 30.9 KD P 1 BETA -(1-3) -GLUCOSYL TR 1 VESICLE COAT PROTEIN S ORF PRECURSOR (FRAGMEN 2 VESICLE COAT PROTEIN S ORF PRECURSOR (FRAGMEN 2 CTG4A. LEUCINE ZIPPER WITH BA 2 LEUCINE ZIPPER WITH BA 2 ELUCINE ZIPPER WITH BA 3 ELUCINE ZIPPER WITH B	AA.  (UPDATE) ON UPDATE)  MAMMALIA; EUTHERIA; (RZCLOWSKI G.P., WIL., (CARE S.A., ANNAN W.I., (SHOURBAGY N.A., BERGS) f hypothalamic neurop late feeding behavior	DB 4; Length 131; 1.03e-143; tches 0; Indels 0; 2PLPDCCRQKTCSCRLYELLHGAGN
060391 040699 0611104 097144 097744 097143 013420 013420 060471 072405 007405 007405 007412 008744 010844 010844 010844 010844 0108412 008844 0108412 008844 0108412 008844 0108412 008844 0108412 008844 010844	NA L L L L L L L L L L L L L L L L L L L	Score 931; Pred. No. 0; Misma LPPALLSSGAAA
901 4 901 10 6 4848 2 486 4 486 4 486 4 5 112 11 3 519 3 1 72 11 1 72 11 1 12 11 1 10 10 1 1139 2 1 1139 2 1 1139 2 1 1139 2 1 1 143 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ELIMINARY;  REMBLREL. 0 REMBLREL. 0 REMBLREL. 0 REMBLREL. 0 AZOA; CHORD MINIDAE; HO MINIDAE; HO W.A. B61. EMIXA A., I EMIXA A., I CENING S.C., UCKINGRAS S.C.,	100.0%; arity 100.0%; Conservative SWAAVTLLLLLL 
22221 22221	44361 11-JUU 11-JUU 11-JUU 11-JUU OMO OMO OMO OMO OMO OMO OMO OMO OMO O	Loc es 1
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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MEDLINE; 98121113.
BEVAN M., BANCROFT I., BENT E., LOVE K., GOODMAN H., DEAN C.,
BERGRAMP R., DIRKSE W., VAN STAVEREN M., STIEKEMA W., DROST L.,
BERGKAMP R., HUDSON S.A., PATEL K., MURPHY G., PIFFANELLI P., WEDLER H.,
WEDLEY E., WAMBUTT R., WEITZENEGGER T., POHL T.M., TERRYN N.,
GIELEN J., VILLARROEL R., DE CLERCK R., VAN MONTAGU M., LECHARNY A.,
AUBORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
BUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                          60 AGILTLGKRRPGPPGLQGRLQRLLQANGNHAAGILTMGRRAGAELEPHPCSGRGCPTVTT 119
                                                                  1 MNFPSTKVPWAAVTLLLLLLL-PPALLSLGVDAQPLPDCCRQKTCSCRLYELLHGAGNHA 59
      Gaps
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DNA RES. 5:169-176(1998).

EMBL: AB014534; D1032570; -.

SEQUENCE 1321 AA: 145424 MW; 4B1721D3 CRC32;
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ISHIKAWA K., NAGASE T., SUYAMA M., MIYAJIMA N., TANAKA A., KOTANI
NOMURA N., OHARA O.;
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      Indels
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SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 74.6 KD PROTEIN.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
13; Mismatches 10;
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Best Local Similarity 57.6%;
Matches 19; Conservative
   Conservative
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107;
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075129
075129;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
598 KYCRSK-YETIHGQNHDNAADVLELAIKREMPAELL-R-ASLRHTNEDQRNFLLNVGRSA 654
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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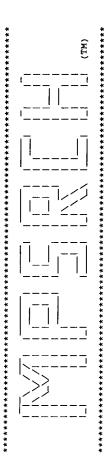
BEMBL; AB005297; DID124528; -.

PERMI; PF00090; LSP_1; 5.

SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;
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MEDLINE; 98208037.
CRAIG A.W.B., HAGHIGHAT A., YU A.T.K., SONENBERG N.;
"Interaction of polyadenylate-binding protein with the eIF4G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.8%; Score 101; DB 4; Length 1584; Best Local Similarity 50.0%; Pred. No. 2.81e-01; Matches 16; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                    / Match 11.1%; Score 103; DB 10; Length 679; Local Similarity 30.6%; Pred. No. 1.60e-01; es 19; Conservative 17; Mismatches 22; Indels
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NO-1-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYADENYLATE BINDING PROTEIN-INTERACTING PROTEIN-I
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                               74635 MW; B301B713 CRC32;
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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102 GA 103
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060455;
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784
790
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                                                                                                                                                                                                                                                                                          LT 14
(01525)
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(01-NOV-1996 (TREMBLREL. 01, CREATED)
(01-NOV-1996 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
(01-NOV-1996 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
(01-NOV-1996 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
HOMO SAPIENS (HUMAN).
SEQUENCE FROM N.A.
MEDLINE, 95086212.
MEDLINE, 95086212.
MOLOUR H., INAZAMA J., NISHIDA J., YAZAKI Y., HIRAI H.;
"Molecular cloning, characterization, and chromosomal localization a novel protein-tyrosine phosphatase, HPTPeta.";
BLOOD 84:4186-4194 (1994).
PROSITE: PSO0383: TYR_PHOSPHATASE_1; 1.
PRAM: PF00102; Y_phosphatase; 1.
SIGNAL; GLYCOPROTEIN, TRANSMEMBRANE; REPEAT; HYDROLASE.
                                                                                                                                      BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
                                                                                                                                                           PROTEIN-TYROSINE PHOSPHATASE ETA. FIBRONECTIN TYPE-III. PROTEIN-TYROSINE PHOSPHATASE.
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                                                                                                                                                                                                                      Length 382;
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BY SIMILARITY.
                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                               Local Similarity 36.7%; Score 95; DB 2; L Local Similarity 36.7%; Pred. No. 1.47e+00; les 11; Conservative 12; Mismatchee
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                                                                                       CREATED)
                                                                                     01-NOV-1998 (TREMBLREL. 08, CREA 01-NOV-1998 (TREMBLREL. 08, LAST 01-NOV-1998 (TREMBLREL. 08, LAST SODIUM DEPENDENT PHOSPHATE PUMP.
                       154 AADDHIAAIALFGNPSG 170
                                   86 ASGNHAAGILTMGRRAG 102
                                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1310 LLSNNGPQASGRLGPTRERGGLPVIEGP-RTGLEASGRGRLGPSRRCSRGRALEPGLASC 1368
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"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA RES. 5:169-176(1998).
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Pred. No. 1.93e+00;
13; Mismatches 28; Indels
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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; D2BA7BB0 CRC32;
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Pred. No. 1.93e+00;
7; Mismatches 6
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Local Similarity 33.8%;
nes 22; Conservative
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les 14; Conservative
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01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 20:52:28 1999; MasPar time 5.99 Seconds 618.331 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-2 (1-131) from US08938548B.pep 931 Description: Perfect Score: Sequence:

1 MNLPSTKVSWAAVTLLLLLLL......GRRCSAPAAASVAPGGQSGI 131

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot37 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.738; Variance 80.369; scale 0.519

# SUMMARIES

Pred. No.	5.91e-03 5.050e-03 7
Description	PROSTAGIANDIN G/H SYNT SECRETIN PRECURSOR (FR TENSIN. TENSIN. PROSTAGIANDIN G/H SYNT PROSTAGIANDIN G/H SYNT PROTEIN-TYROSINE PHOSP ADENYLATE CYCLASE, TYP URIDINE KINASE (EC 2.7 PROSTAGIANDIN G/H SYNT HYPOTHETICAL 22.7 KD P GROWTH REGULATED PROTE HYPOTHETICAL PROTEIN K PROTEIN-TYROSINE PHOSP CATION-INDEPENDENT MAN RETINAL GUANYLYL CYCLA SIC CYTOKINE PRECURSOR COMPLEMENT CIQ SUBCOM SEX HORMONE-BINDING GIL TRANS-ACTING TRANSCRIP STRANS-ACTING TRANSCRIP
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Length	131 1347 1347 1313 1313 1313 1313 1313 1
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PERULT 1  D FGH1_ENG  DD FGH1_ENG  DD FGH1_ENG  G63921; G62731; G65884;  DT 15-DEC-1998 (REL. 37, CREATED)  DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)  DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)  DE FORDEALDANIN GIA SYNTHASE I PREURENCE (EC 1.14.99.1) (CYCLOOXYGENASE SYNTHASE I) (PGH SYNTHASE I) (PGHS-1) (PHS 1).  GN PTGS1 OR COX1 ON COX1 (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE I) (PGHS-1) (PHS 1).  GN PTGS1 OR COX1 (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE I) (PGHS-1) (PHS 1).  CHARTOTA, METAZOA, GHORDATA, VERTEBRATA; MAMMALIA; EUTHERIA;  CRODENTA, SCHINCONAHII; MURIDAE; MURINAE; RATTUS.  RATTUS NORVEGICES (RAT).  CRODENTA, SOLUTION AND D.;  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RA FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,  RACH. BIOCHEM. BIOCHEM. BIOPHYS. 307:361-368(1993).  RACH. BIOCHEM. BIOPHYS. 307:361-368(1993).  RA RILEGAL SA MAY PLAY AN INFORMAL AND NEOPLASTICALLY TRANSFORMED  CC CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED  CC THROMBOLYNES.  CC THROMBOLYNE		CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL 38.7 KD PROTEIN IN TKTB-NARQ INTERGENIC REGION PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LLFFFALLPTSLVWAAPAQRAFSD--WQVTCNNQNFCVARNTGDHNGLVMTLSRSAGAHT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                      18
56 SECRETIN.
56 AMIDATION (G-57 PROVIDE AMIDE GROUP).
14277 MW; 837D201A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACIERIA; PROTEOBACIERIA; GAMMA SUBDIVISION; ENTEROBACIERIACEAE;
ESCHERICHIA.
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                                                                                                                                                                            Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.3%; Score 105; DB 1; Length 347; Best Local Similarity 25.0%; Pred. No. 1.09e-02; Matches 17; Conservative 29; Mismatches 20; Indels
                                                                                                                                             Score 107; DB 1; Length ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
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PFAM; PF00123; hormone2; 1.
HSSP; P01274; 1GCN.
GLUCAGON FAMILY; HORMONE; AMIDATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                    347 AA
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72.7%;
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STRAIN-K12 / MG1655;
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-I-FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON. BINDS TO ACTINN AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES.

-I-SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.

-I-TISSUE SPECIFICITY: HEART, GIZZARD, LUNG AND SKELETAL MUSCLE.

-I-PIM: TYROSINE-PHOSPHORYLATED.

-I-SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                           MEDITINE; 94350987.
LO S.H., AN Q., BAO S., WONG W.K., LIU Y., JANMEY P.A., HARTWIG J.H.,
                                                                                                                                                                                                                                                                                                                   "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence, expression, and characterization.";
J. BIOL. CHEM. 269:22310-22319(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 91220073.
DAVIS S., LU M.L., LO S.H., LIN S., BUTLER J.A., DRUKER B.J.,
ROBERTS T.M., AN Q., CHEN L.B.;
"Presence of an SH2 domain in the actin-binding protein tensin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAN DE WERKEN R., GENNARI M., TAVELLA S., BET P., MOLINA F., LIN S., CANCEDDA R., CASTAGNOLA P.; Modulation of tensin and vimentin expression in chick embryo developing carrilage and cultured differentiating chondrocytes."; EUR. J. BIOCHEM. 217:781-790(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 95204530.
CHUANG J.Z., LIN D.C., LIN S.;
Molecular cloning, expression, and mapping of the high affinity actin-capping domain of chicken cardiac tensin.";
J. CELL BIOL. 128:1095-1109(1995).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH2 DOMAIN; PHOSPHORYLATION. TENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN L.B.;
SUBMITTED (XXX-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=EMBRYONIC CHONDROCYTES, AND EMBRYONIC HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH2.
C -> R (IN REF. 2
M -> T (IN REF. 2
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EMBL; L06662; G212755; ALT_INIT.
EMBL; 218529; G63805; ALT_INIT.
EMBL; M74165; G212752; ...
EMBL; X66286; G63803; -..
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1469-1744 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00017; SH2; 1.
HSSP; P16277; 1BLJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94039118.
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TISSUE PANCREATIC ISLETS;

MEDLINE; 97254813.

A MEDLINE; 97254813.

A SHEPPARD P., KINDSVOGEL W., HAGOPIAN W.A.;

The 37-kDa autoantigen in type 1 diabetes: human and macaque acquences, tissue distribution, unique and shared epitopes, and predictive autoantibodies.";

MOL. MED. 3:163-173(197).

C -!- FUNCTION: IMPLICATED IN DEVELOPMENT OF NERVOUS SYSTEM AND PANCREATIC ENDOCRINE CELLS.

C -!- CTALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 = PROTEIN TYROSINE + ORRHOPBEATE).
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                                                                 Gaps
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TISSUE SPECIFICITY: BRAIN, PROSTATE, PANCREATIC ISLETS. LOWER
EXPRESSION IN SPINAL CORD, THYROID, ADRENAL MEDULLA AND
                                                                                                                                                                                                                                                                              PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONSECUTIVE BASIC RESIDUES (BY SIMILARITY).
SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
                                                                                                                                                                                                                                                                                                                             MACACA NEMESTRINA (PIG-TAILED MACAQUE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
                                                                   ..
H
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PTM: APPEARS TO UNDERGO MULTIPLE PROTEOLYTIC CLEAVAGE AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN-TYROSINE PHOSPHATASE X. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE SITE (BY SIMILARITY)
                               Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN-TYROSINE PHOSPHATASE
                            Score 101; DB 1; Length 599
Pred. No. 4.00e-02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASE; RECEPTOR; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9EC7D263 CRC32;
68656 MW; 8C7684CD CRC32;
                                                                                                                                                                                                                             01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                 PRT; 1013 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U91574; G1916942; -.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
PFAM: PF00102: Y_phosphatase: 1.
HSSP; P18052; 1YFO.
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                            Query Match 10.8%;
Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                                                                                                                               STANDARD;
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562 56
1013 AA;
599 AA;
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PTPX_MACNE
002695;
SEQUENCE
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ACT_SITE
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CARBOHYD
                               Query Match
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DOMAIN
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Score 99; DB 1; Length 1013;

10.6%;

Query Match

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SMITH P.D., BARKER K.T., WANG J., LU Y.-J., SHIPLEY J., CROMPTON M.R.; "ICAAR, a novel member of a new family of transmembrane, tyrosine phosphatase-like proteins.";
BIOCHEM. BIOPHYS. RES. COMMUN. 229:402-411(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
TISSUE=BRAIN, AND PANCREAS;
MEDLINE; 96394649.
GUI L., YU W.-P., DE ALZPURUA H.J., SCHMIDLI R.S., PALLEN C.J.;
"Cloning and characterization of islet cell antigen-related protein-tyrosine phosphatase (PTP), a novel receptor-like PTP and autoantigen in insulin-dependent diabetes.";
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILNE; 97032784.

KAWASAKI E., HUTION J.C., EISENBARTH G.S.;

"Molecular cloning and characterization of the human transmembrane protein tyrosine phosphatase homologue, phogrin, an autoantigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PANCREATIC ENDOCRINE CELLS. OPTIMUM ACTIVITY IS MEASURED AT PH
                                                                                                                                                                                                                                                                          PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DISEASE: AUTOANTIGEN IN INSULIN-DEPENDENT DIABETES MELLITUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN TYROSINE + ORTHOPHOSPHATE.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).

-!- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND PANCREAS.

-!- LEVELS IN TRACHEA, PROSTATE, STOMACH AND STINAL CHORD.

-!- PTM: APPEARS TO UNDERGO MULTIPLE PROTEOLYTIC CLEAVAGE AT
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOL. CHEM. 271:24817-24823(1996).
- FUNCTION: IMPLICATED IN DEVELOPMENT OF NERVOUS SYSTEM AND
                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRINATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONSECUTIVE BASIC RESIDUES.
DOMAIN: THE CYTOPLASMIC DOMAIN APPEARS TO CONTAIN THE
                      Indels
Best Local Similarity 57.1%; Pred. No. 7.56e-02; Matches 12; Conservative 7; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHEM. BIOPHYS. RES. COMMUN. 227:440-447(1996)
                                                                                                                                          RESULT 7

ID PTPX_HUMAN STANDARD; PRT; 1010.02922; Q92662;

AC Q92932; Q92662;

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 36, LAST ANNOTATION UPDATE)
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                                                                                              LLLLLLLPPALLSSGAAAOP
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                                                          6 LLLLLLLLPPRVLPAAPSSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=FETAL BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 1 diabetes
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US-08-938-548B-2.rsp

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GRO_CRIGR
P09340;
   CHAIN
DOMAIN
ACT_SITE
ACT_SITE
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DISULFID
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   (See http://www.isb-sib.ch/announce/
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01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE
-1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN H2
SXNTHASE 1) (PGH SYNTHASE 1) (PGHS-1) (PHS 1).
PTG31 OR COX1 OR COX-1.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 90203007.

DEWITT D.L., EL-HARITH E.A., KRAEMER S.A., ANDREWS M.J., YAO E.F.,
ARMSTRONG R.L., SMITH W.L.;

The aspirin and heme-binding sites of ovine and murine prostaglandin
endoperoxide synthases.";

J. BIOL. CHEM. 265:5192-5198(1990).

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING
CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE. HIS BRIXTME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE. THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) = PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXIDOREDUCTASE; DIOXYGENASE; PEROXIDASE; GLYCOPROTEIN; ACETYLATION; PROSTAGLANDIN BIOSYNTHESIS; HEME; IRON; SIGNAL; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H2 + A + H(2)O. PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                           ;
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                   Score 97; DB 1; Length 260;
Pred. No. 1.42e-01;
14; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   218 LCKRHRGGPNGRNH-KRTFPEPGDHP-GVLATGKRSHLESSSRP 259
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260 AA; 29622 MW; E72BB622 CRC32;
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entities requires a license agreement (Sont send an email to license@isb-sib.ch).
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PROSITE; PS01186; EGF_2; FALSE_NEG-
PFAM; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 34.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M34141; G200303; -.
                                                                                        EMBL; L31783; G471981; -.
MGD; MGI:98904; UMPK.
TRANSFERASE; KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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MGD; MGI:97797; PTGS1
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PGH1_MOUSE
P22437;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                      DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
ASPIRIN-ACETYLATED SERINE.
BY SIMILARITY.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKL147C OR YKL601.
SACCHAROWYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
HYPOTHETICAL 22.7 KD PROTEIN IN SHIL-CIMS/YTA3 INTERGENIC REGION
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PROSTAGLANDIN G/H SYNTHASE 1.
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Pred. No. 1.94e-01;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Score 97; DB 1; Length 602;
Pred. No. 1.42e-01;
7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
96489281 CRC32;
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PIR; S44581; S44581.
PLOTHETICAL PROTEIN.
SEQUENCE 205 AA; 22673 MW; 0AEA8D4E CRC32;
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                                                                                                                                                                                                                                                                                                                                                69042 MW;
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Best Local Similarity 53.8%;
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Best Local Similarity 38.7%;
Matches 12; Conservative
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01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (CI MAN-6-P
RECEPTOR) (CI-MPR) (INSULIN-LIKE GROWTH FACTOR II RECEPTOR).
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 88115411.
LOBEL P., DAHMS N.M., KORNFELD S.;
"Cloning and sequence analysis of the cation-independent mannose 6-phosphate receptor.";
phosphate receptor.";
J. BIOL. CHEM. 263:2563-2570(1988).
                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                                                                                                                                                                                                                                                                            BOS TAURUS (BOVINE).
EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                          Score 94; DB 1; Length 1337;
Pred. No. 3.59e-01;
                                                                                                                                                                                                                                                                                        Indels
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W: 55F90A6B CRC32;
                                BY SIMILARITY.
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Similarity 48.3%;
14; Conservative
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666
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                                           FECEPTOT.";

PROC. NATL. ACAD. SCI. U.S.A. 84:2233-2237(1987).

PROC. NATL. ACAD. SCI. U.S.A. 84:2233-2237(1987).

-:- FUNCTION: TRANSPORT OF PHOSPHORILATED LYSOSOMAL ENZYMES FROM THE GOLGI COMPLEX AND THE CELL STRFACE TO LYSOSOME. LYSOSOMAL ENZYMES BEARING PHOSPHOMANNOSYL RESIDUES BIND SPECIFICALLY TO MANNOSE-6-PHOSPHORE RECEPTORS IN THE GOLGI PAPPARATOR AND THE RESULTING RECEPTOR-LIGAND COMPLEX IS TRANSPORTED TO AN ACIDIC PRELYOSOMAL COMPARTMENT WHERE THE LOW PH MEDIATES THE DISSOCIATION OF THE COMPLEX. THIS RECEPTOR ALSO BINDS INSULIN GNOWTH FACTOR II.

-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. LYSOSOMAL.

-:- DOMAIN: CONTAINS 15 REPRATING UNITS OF APPROXIMATIVELY 147 AA. THE MOST HIGHLY CONSERVED REGION WITHIN THE REPEAT CONSISTS OF A STRETCH OF 13 AA THAT CONTAINS CYSTEINES AT BOTH ENDS.
                        'Cloning of the bovine 215-kDa cation-independent mannose 6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. . CATION-INDEPENDENT MANNOSE-6-PHOSPHATE
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Fransmembrane; transport; glycoprotein; repeat; receptor: lysosome
  KORNFELD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
COBEL P., DAHMS N.M., BREITMEYER J., CHIRGWIN J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-II.
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PIR; A30788; A30788.
PROSITE; PS00023; FIBRONECTIN_2; 1.
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PFAM; PF00878; CIMR_repeat; 12.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 20:51:49 1999; MasPar time 8.66 Seconds 606.456 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-2 (1-131) from USO8938548B.pep 931 1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAASVAPGGQSGI 131

Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 40.416; Variance 87.828; scale 0.460 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Pred. No.	9.52e-03	1.29e-02	1.75e-02	2.36e-02	2.36e-02	4.29e-02	7.76e-02	7.76e-02	1.04e-01	1.04e-01	1.39e-01	1.39e-01	1.39e-01	2.49e-01	2.49e-01	2.49e - 01	3.32e-01	4.41e-01	5.86e-01	5.86e-01	7.77e-01	7.77e-01	1.03e+00
Description	hypothetical protein	prostaglandin G/H syn	prostaglandin-endoper	secretin precursor -	cyclooxygenase 1 - ra	hypothetical protein	hypothetical protein	tensin - chicken (fra	tensin - chicken	tensin, cardiac muscl	prostaglandin-endoper	prostaglandin-endoper	brain-specific anglog	FLT3/FLK2 ligand (clo	phogrin precursor - h	transmembrane tyrosin	adenylate cyclase (EC	prostaglandin-endoper	hypothetical protein	hypothetical protein	probable cutinase pre		
ΩI	T00382	869198	A36746	SEPG	S39782	A65022	C71413	A57075	S27939	A54970	A38146	JH0259	T00026	S43293	JC5062	JC5263	A49201	A35564	S37804	A61183	A70565	JC6197	B28414
DB	7	7	7	П	7	7	7	~	7	7	~	7	~	7	7	~	~	~	7	7	7	7	7
& Query Match Length	1321	602	599	131	602	347	619	1792	1733	1744	295	299	1584	245	1015	1015	1166	602	202	312	226	491	101
& Query Match	11.8	11.7	11.6	11.5	11.5	11.3	11.1	11.1	11.0	11.0	٠.		10.8	10.6	10.6	10.6	10.5	10.4	10.3	10.3	10.2	10.2	10.1
Score	110	109	108	107	107	105	103	103	102	102	101	101	101	66	66	66	86	6	96	96	95	95	94
Result No.	П	7	ю	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.03e+00	1.03e+00	1.03e+00	1.79e+00	1.79e+00	1.79e+00	1.79e+00	1.79e+00	1.79e+00	2.36e+00	3.10e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	5.32e+00
protein-tyrosine-phos	hypothetical protein	mannose 6-phosphate r	Flt3 ligand alternati	flt3 ligand - human	FLT3/FLK2 ligand (clo	complement subcompone	immediate-early prote	immediate-early prote	stromelysin 3 (EC 3.4	hypothetical protein	heat-stable antigen M	gene E protein - phag	lysis protein - phage		FLT3/FLK2 ligand (clo	flt3 ligand isoform 5	flt3/flk-2 ligand pre	hypothetical protein	serine proteinase sna	phosphatidylcholine	triacylglycerol lipas
138670	T00391	A30788	139076	I38440	S43292	CIHUQB	EDBE22	EDBE23	A44399	S24303	A43537	ZEBPF4	S47060	JS0455	S43291	I58343	A49265	G64151	A24702	XXMSN	S28225
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94	8	94	6	92	92	95	92	92	91	90	8	8	83	83	8	8	8	83	8	8	88
24	25	56	27	28	29	30	31	32	33	34	35.	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT

ENTRY	T00382 #tvbe fragment
TITLE	etica
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
	01-Feb-1999
ACCESSIONS	T00382
REFERENCE	214142
#authors	Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka,
	A.; Kotani, H.; Nomura, N.; Ohara, O.
#journal	DNA Res. (1998) 5:169-176
#title	Prediction of the coding sequences of unidentified human
	genes. X. The complete sequences of 100 new cDNA clones
	from brain which can code for large proteins in vitro.
#accession	T00382
##status	preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA	type mRNA
##residues	1-1321 ##label ISH
##cross-ref	##cross-references EMBL;AB014534; NID:d1204289; PID:d1032570
##experimer	##experimental_source brain
GENETICS	
#note	KIAA0634
SUMMARY	#length 1321 #checksum 8342
Query Match 11.8%;	11.8%; Score 110; DB 2; Length 1321;
Best Local Simi	Pred. No. 9.52e-03;
Matches 19;	19; Conservative 7; Mismatches 4; Indels 3; Gaps 3;

셤 ò S69198 #type complete

#formal\_name Rattus norvegicus #common\_name Norway rat
#formal\_name Rattus norvegicus #common\_name Norway rat
24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change
10-Sep-1997
S69198; Kitzler, J.W. submitted to the EMBL Data Library, December 1994 S69198 #submission #accession ##status #authors ACCESSIONS REFERENCE RESULT ENTRY TITLE ORGANISM DATE

##molecule\_type mRNA ##residues 1-602 ##label KIT

preliminary

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4

Length 679;

DATE

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Analysis of 1.9 Mb of contiguous sequence from chromosome 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Chuang, J.Z.; Lin, D.C.; Lin, S.
#journal J. Cell Biol. (1995) 128:1095-1109
#title Molecular cloning, expression, and mapping of the high
affinity actin-capping domain of chicken cardiac tensin.
#cross-references MUID:95204530
                                                                                                                                         ##residues
##cross-references GB:Z97337; NID:g2244829; PID:e326841; PID:g2244855
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                                                                                                                                                                                                                                                                                                                                                                                     Score 103; DB 2; Length 1792;
Pred. No. 7.76e-02;
13; Mismatches 22; Indels 4; Gaps
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#formal_name Gallus gallus #common_name chicken
05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change
12-Feb-1999
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MARX #length 679 #molecular-weight 74635 #checksum 9028
                                                                                 nucleic acid sequence not shown
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Pred. No. 7.76e-02;
17; Mismatches 22;
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#length 1792 #checksum 2643
                                                                                                         translation not shown
                   of Arabidopsis thaliana 
#cross_references MUID:98121113
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##residues 1-1792 ##label CHU
                                                                               preliminary;
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Local Similarity 30.6%;
hes 19; Conservative
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Best Local Similarity 38.1%;
Matches 24; Conservative
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                                                                                                                          ##molecule_type DNA
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                                                                                                                                                                                                                                                                   A65022
A64120
Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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1;
                                                                                                                                             A65022 #type complete
hypothetical protein b2466 - Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-sep.1997 #sequence_revision 17-Sep-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references GB:AE000333; GB:U00096; NID:g1788805; PID:g1788809; UMGP:b2466
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hypothetical protein - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain K-12, substrain MG1655
Y #length 347 #molecular-weight 38746 #checksum 7897
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2;
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Pred. No. 4.29e-02;
29; Mismatches 20; Indels
Indels
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6; Mismatches
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                                      12 LLLLLLLPPPPVLLTDAGVPSPVIPCC 39
                                                                Query Match
Best Local Similarity 25.0%;
Matches 17; Conservative
Conservative
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                                                                                                                                                                                                                                       #Journal Diaz, A.; Reginato, A.M.; Jimenez, S.A.
#journal J. Biol. Chem. (1992) 267:10816-10822
#title Alternative splicing of human prostaglandin G/H synthase mRNA and evidence of differential regulation of the resulting transcripts by transforming growth factor beta 1, interleukin 1 beta, and tumor necrosis factor alpha.
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Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.;
Kiyono, K.; Tatsumi, K.; Yoshida, S.; Ono, M.; Kuwano, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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Chan, Biophys. Acta (1994) 1209:130-139
Purification, characterization and selective inhibition of human prostaglandin G/H synthase 1 and 2 expressed in the
                                 Fitzgerald, G.A.
FASEB J. (1991) 5:2304-2312
Human platelet/erythroleukemia cell prostaglandin G/H
synthase: cDNA cloning, expression, and gene chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain signal sequence #status predicted #label SIGN #product prostaglandin-endoperoxide synthase #status experimental #label MAT #arental #label MAT #length 599 #molecular-weight 68656 #checksum 4138
                                                                                                                                                                                                                                                                                                                                                                                                                This enzyme is bifunctional with the fatty acid cyclooxygenase activity and prostaglandin hydroperoxidase activity.
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22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
12-Feb-1999
                   Funk, C.D.; Funk, L.B.; Kennedy, M.E.; Pong, A.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brain-specific angiogenesis inhibitor 1 - human
BAI1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 2; Length 599 Pred. No. 1.39e-01;
                                                                                                                                                                   ##residues 1-599 ##label FUN
##cross-references GB:M59979; NID:g189886; PID:g189887
Phose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GDB:128070; OMIM:176805
#map_position 9932-9933.3
WORDS alternative splicing; oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type protein
##residues 24-32 ##label BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 baculovirus system.
#cross-references MUID:95035046
                                                                                                              assignment.
#cross-references MUID:91317397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 51.9%;
hes 14; Conservative
                                                                                                                                                                   ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB: PTGS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S50181
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                                                                                                                                                   A39937
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                                                                                                                                                                                      ##residues
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                                                                                                                                                 #accession
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                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                      #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
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24-599
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REFERENCE
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Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kastelein, R.; Hudak, S.; Wagner, J.; Mattson, J.; Luh, J.; Duda, G.; Martina, N.; Peterson, D.; Menon, S.; Shanafelt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.; Rosnet, O.; Dubreull, P.; Birnbaum, D.; Lee, F. Nature (1994) 368:643-648

Jigand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by
                                                                                                                                                                                                                                                                                                                                                    #domain thrombospondin type 1 repeat homology #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-245 ##label HAN
the authors translated the codon AGT for residue 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phogrin precursor - human
protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S43293 #type complete
FLT3/FLK2 ligand (clone $109) - human
#formal_name Homo sapiens #common_name man
20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         #checksum 7909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length 245 #molecular-weight 27404 #checksum 295
                                                                                                                                                                                                                                                                  #map_position 8q24-8q24
CLASSIFICATION #superfamily thrombospondin type 1 repeat homology
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                                                                                                     ##residues 1-1584 ##label NIS ##cross-references EMBL:AB005297; NID:d1175078; PID:d1024528
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1584;
submitted to the EMBL Data Library, June 1997 T00026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; DB 2; Length 245;
Pred. No. 2.49e-01;
9; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                THR3
#length 1584 #molecular-weight 173531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawasaki, E.; Hutton, J.C.; Eisenbarth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB 2;
Pred. No. 1.39e-01;
                                                      translated from GB/EMBL/DDBJ
                                                                                                                                                                                                              ne GDB:BAIl
##cross-references GDB:9838088; OMIM:602682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 WILAPLLLLLLLGRRARAAGADAGPGPEPC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 WAAVTLLLLLLL-PPALLSSGAAAQPLPDCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                               ##experimental_source brain
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Best Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 SWAAVTLLLLLLLDPPALLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AWSPTTYLLLLLLLSSGLMGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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##residues 1-249
                                                                               ##molecule_type mRNA
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<b>植物植物植物植物植物植物植物植物植物植物 医水体性 医克里特氏征 医克里特氏试验检尿道 医克里特氏试验检尿道 医克里特氏试验检尿道 医克里特氏试验检尿道 医二甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基</b>	·=====================================
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MasPar time 6.37 Seconds 239.851 Million cell updates/sec Fri Aug 20 20:58:15 1999; Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Tabular output not generated.

>US-08-938-548B-4 (1-28) from US08938548B.pep 196 1 RSGPPGLQGRLQASGNHAAGILIM 28 Title:

Description: Perfect Score:

PAM 150 Gap 15 Scoring table:

Sequence:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus sptremb19 Database:

Mean 30.076; Variance 50.517; scale 0.595 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Pred. No.	1.42e-25	6.55e-25	3.01e-24	3.01e-24	2.25e-01	1.45e+00	2.09e+00	2.09e+00	3.00e+00	3.00e+00	3.00e+00	4.29e+00	4.29e+00	4.29e+00	4.29e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00
Description	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	TIGHT JUNCTION PROTEIN	T13D8.6 PROTEIN.	K+ CHANNEL BETA4 SUBUN	PAR INTERACTING PROTEI	HRPE.	ARTICULIN P60.	H06001.2 PROTEIN.	RNA POLYMERASE SIGMA-L	YONC PROTEIN.	HYPOTHETICAL 19.6 KD P	RETINOID X RECEPTOR IN	T9J22.21 PROTEIN.	RNA POLYMERASE SIGMA-L	D-SUBUNIT OF BENZOYL-C	RNA POLYMERASE SIGMA F	RNA POLYMERASE SIGMA F
А	043612	077668	055241	055232	095168	080740	P97382	035821	052495	027212	017909	085680	031955	064066	060811	048721	085683	087877	P95644	Q59913
& Query Match Length DB	131 4	131 6	130 11	130 11	1174 6	511 10	249 11	1277 11	439 2	568 5	1465 5	162 2	178 2	178 9	580 11	145 10	161 2	282 2	462 2	510 2
Query	100.0	98.5	6.96	6.96	38.8	36.2	35.7	35.7	35.2	35.2	35.2	34.7	34.7	34.7	34.7	34.2	34.2	34.2	34.2	34.2
Score	196	193	190	190	16	71	70	70	69	69	69	68		68	68	67	67	67	67	67
Result No.	-1	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20

6.12e+00 6.12e+00 6.12e+00	6.12e+00	6.12e+00 6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	8.69e+00	8.69e+00	8.69e+00	8.69e+00	8.69e+00	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.73e+01	1.73e+01
MAJOR VEGETATIVE SIGMA RNA POLYMERASE SIGMA F RNA POLYMERASE SIGMA F	POLYMERASE SIGMA	HYPOTHETICAL 60.1 KD P POLYPROTEIN.	VP2, NS, VP3.	PUTATIVE ABC TRANSPORT	TYLACTONE SYNTHASE MOD	NUMA PROTEIN.	PRISTINAMYCIN I SYNTHA	TNA2, TNA1, PARTIAL AN	LEUCINE ZIPPER WITH BA	STEROID 21-HYDROXYLASE	KIAA0566 PROTEIN (FRAG	P160 MYB-BINDING PROTE	MOUSE 57-KD CALCIUM-BI	HYPOTHETICAL 33.8 KD P	3-HYDROXYISOBUTYRYL-CO	TRANSCRIPTIONAL ACTIVA	F14D7.2 PROTEIN.	HYPOTHETICAL 55.5 KD P	OXOGLUTARATE DEHYDROGE	ORF263.	HSGAK.
050539 P77951 Q59813	059814	069851 P89521	055651	081016	033958	014980	054959	050648	091640	054797	060312	035851	062041	033744	092931	050205	019452	042651	049541	031722	014976
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511 514 525	528	541 972	972	1420	1841	2115	2591	213	331.	490	1163	1344	178	312	381	443	457	481	973	263	1311
34.2 34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.2	33.7	33.7	33.7	33.7	33.7	33.2	33.2	33.2	33.2	33.2	33.2	33.2	32.7	32.7
67 67 67	67	67	29	67	29	67	29	99	99	99	99	99	65	9	65	9	, 59	65	65	64	64
21 22 23	24	25 26	27	28	29	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1  PREJIT 1  O43612,  AC 043612,  DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  DE PREPRO-OREXIN.  CS HOWO SAPIENS (HUMAN).  CC CATARRHINI, HOMINIDAE; HOMO.  RN [1]  RA SEQUENCE FROM N.A.  RA SAKURAI T., AMEMIYA A., ISHII M., MATSUZAKI I., CHEMELLI R.M.,  RA TANAKA H., WILLIAMS S.C., RICHARDSON J.A., KOZLOWSKI G.P., WILGON S.,  RA ARCH J.R.S., BUCKINGHAM R.E., HAYNES A.C., CARR S.A., ANNAN R.S.,  RA ARCH J.R.S., BUCKINGHAM R.E., HAYNES A.C., CARR S.A., ANNAN R.S.,  RA ARCH J.R.S., BUCKINGHAM R.E., HAYNES A.C., CARR S.A., ANNAN R.S.,  RA ARCH J.R.S., BUCKINGHAM R.E., HAYNES A.C., CARR S.A., BUCKINGHAM R.E., LIU WS., TERRETT J.A., ELSHOURBAGY N.A., BERGSMA D.J.,  RA TANAGISAWA M.;  "Orexins and orexin receptors: a family of hypothalamic neuropeptides  RT and G protein-coupled receptors that regulate feeding behavior.";  RR EMBL, AF041240; G2897118;  SG SEQUENCE 131 AA; 13363 MW; 2C11048A CRC32;
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Pred. No. 1.42e-25; 0; Mismatches 0; Indels Local Similarity 100.0%; es 28; Conservative Best Loc Matches

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Gaps

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Gaps

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Indels

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Pred. No. 1.45e+00;
                                           330
                                                                  23
                                                           308 QSTPPGLQARAGRLVAAKSTLAA
                                                                                                    RESULT 7
1D P97382,
AC P97382,
DT 01-MAY-1997 (TREMBLREL. 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 35.7%;
Best Local Similarity 25.9%;
Matches 7; Conservative
         Best Local Similarity 52.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                             35.7%;
Similarity 81.8%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             23 PPGLQGSLDRL 33
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                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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035821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARABIDOPSIS THALLANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACERE; ARABIDOPSIS.
                                                               BEATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.; "The tight junction protein ZO-2 contains three PDZ (PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced region."; J. BIOL. CHEM. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA,
VYSOTSKAIA V.S., SCHWARTZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
LIU S., LI J., ARRUJO R., AU M., BRENDEL V., BUEHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURTZ D., LI Y., PALM C.J.,
SHINN P., SUN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A.,
THEOLOGIS A.,
"Arabidopsis thaliana chromosome I BAC T13D8 sequence.";
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                   Length 1174;
                                                                                                                                                                                                                                                                                Query Match 38.8%; Score 76; DB 6; Length 1174 Best Local Similarity 35.7%; Pred. No. 2.25e-01; Matches 10; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                             BEATCH M.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
BUBL; 127152; G1556970; -.
PFAM; PF00595; PDZ; 3.
PFAM; PF00625; Guanylate, Xin; 1.
SEQUENCE 1174 AA: 132085 MW; 2FA16B83 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THEOLOGIS A.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                   GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55547 MW; 70D6FDB7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                      511 AA
                                                                                                                                                                                                                                                                                                                              268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295
                                                                                                                                                                                                                                                                                                                                            CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
         tumor suppressor protein.";
J. CELL BIOL. 124:949-961(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                           08,
08,
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SEQUENCE 511 AA; 55547
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA; THEOLOGIS;
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STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. COLUMBIA;
THEOLOGIS A.;
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                         SEQUENCE FROM N.A. MEDLINE; 96421547.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             T13D8.6 PROTEIN.
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080740
080740;
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Length 511;

DB 10;

36.2%; Score 71;

Query Match

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                                                                                                                  K+ CHANNEL BETA4 SUBUNIT.
MUS MUSCULUS (MOUSE).
EUKARXOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MUSINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91084854.

WUARIN J., SCHIBLER U.;

"Expression of the liver-enriched transcriptional activator protein
DBP follows a stringent circadian rhythm.";
CELL 63:1257-1266(1990).
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                                                                                                                                                                                                                                                                                                                                  LAZDUNSKI M.;
"A new K+ channel beta subunit to specifically enhance Kv2.2 (CDRK)
                                                                                                                                                                                                                                                                                      MEDLINE; 96421640.
FINK M., DUPRAT F., LESAGE F., HEURTEAUX C., ROMEY G., BARHANIN J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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SUBMITIED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U83590; G2253211; -
SEQUENCE 1277 AA; 144674 MW; 89721F79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                          01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 11; Pred. No. 2.09e+00; 16; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 11; Pred. No. 2.09e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA; 27749 MW; 8805DBE7 CRC32;
249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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05, LAST SEQU
08, LAST ANNO
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J. BIOL. CHEM. 271:26341-26348(1996).
EMBL; U65593; G1695272; -.
IONIC CHANNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SGPPGLQGRLQARLLQASGNHAAGILTM 28
PRT;
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AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORGISER L., BRANS A., BRANN M., BRIGHELL S.C., BRON S.,
BROUILLET S., BOURELLER L., BRANS A., BRANN M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BROUILLET S., BERINGTON J., FEBRET C., FERRARI E., FOULGER D.,
BROUILLET S., CODANI J.J., FOUNT Y., FUNA S., GALIZIZI A., GALICERON N.,
BRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZIZI A., GALICERON N.,
BRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZIZI A., GALICERON N.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HOLLO M.F., ITAYA M., JONES L.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HOLLO M.F., ITAYA M., JONES L.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HOLLO M.F., ITAYA M., JONES L.,
A HILBERT H., HOLSAPPEL S., KONINGSTEIN G., KROGH S., KUMANO M.,
A HILBERT H., HOLSAPPEL S., CANINGSTEIN G., ROGH S., KUMANO M.,
A HILBERT H., HOLSAPPEL S., SOUNINGSTEIN G., ROGH S., KUMANO M.,
A HILBERT H., HOLSAPPEL S., SOUNINGSTEIN G., ROGH S., NOBACK M.,
A NOBLE D., O'RELLLY M., PORTEFELLE D., PORMOLLIK S., PRESCOTT A.M.,
A RESER M., RIVOLTA C., ROCHA E., ROCHE B., PARK S.H.,
A REGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
A REGER M., TARGONI E., SEROR S.J., SERROR P., SHIN B.S., SOLDO B.,
SEXIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., TARREMBRU K.,
A TAREUCHI M., TARAKOSHI A., TARAKOSHI R., YABABNIT R., WEDLER H., WELLER H., WEDLER H., WEDLER H.,
A TOSATO V., UCHITAMA S., VANDENBOL M., VANDEN P., VASSAROTTI A.,
A TOSATO V., UCHITAMA S., VANDENBOL M., VANDEN P., TACONI E.,
A TOSHIDA R., YABABNOTO H., YABABNE R., YASSUMOTO K., YATA R.,
A WINTERS P., WIPAT A., YAMAMOTO H., YABABNE R., YOSHIDA R., YOSHIRAWA H., P., ZOMSTEIN E., YOSHIRAWA H., DANCHIN S.,
A SHILLIS P., WIPAT A., YABABNOTO R., YASSUMOTO K., YASSUMOTO R., YOSHIRAWA H., P., ZOMSTEIN P., YOSHIRAWA H., DANCHIN S.,
A SHARLING R., YOSHIRAWA H., P., ZOMSTEIN P., YOSHIRAMA H., DANCHIN S.,
A SHARLING
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BACILLUS.
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                                                                                                                                                                                                                                                             Score 68; DB 2; Length 162;
Pred. No. 4.29e+00;
10; Mismatches 4; Indels
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Pred. No. 4.29e+00;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                          4; Indels
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SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z99115; E1183561;
SEQUENCE 178 AA; 19609 MW; CA7B8EDO CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                    162 AA; 18499 MW; 633A3527 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 AA
from Actinomycetes.";
... MICROBIOL. BIOTECHNOL. 8:280-283(1998).
EMBL: AF071792; G3249723; -..
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                    111 LODQLQQVLQTLSEREAGVVRL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LOGRLDARLLQASGNHAAGILTM 28
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05,
08,
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.4%;
Matches 8; Conservative
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Best Local Similarity 45.0%;
Matches 9; Conservative
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                                                                                                                                                      162
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MEDLINE; 98044033
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SEQUENCE
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031955
031955;
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95280959.
SEOL W., CHOI H.S., MOORE D.D.;
SEOL W., CHOI H.S., MOORE D.D.;
"Isolation of proteins that interact specifically with the retinoid X receptor: two novel orphan receptors.";
MOL. ENDOCRINOL. 9:72-85(1995).
EMBL; U22015; G709961; --
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
LAZAREVIC V., DUESTERHOEFT A., SOLDO B., HILBERT H., MAUEL C.,
KARAMATA D.;
SUBMITTED (40G-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF020713; G3025531;
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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Pred. No. 4.29e+00;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 9; Length 178; Pred. No. 4.29e+00; 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RETINOID X RECEPTOR INTERACTING PROTEIN 110 (FRAGMENT).
                                                                                                                                                                             01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 19-6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA; 64852 MW; 28DA7406 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 AA; 19609 MW; CA7B8ED0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 AA
                                                                                                                                     178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: Fri Aug 20 20:58:42 1999 Job time : 27 secs.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANNO
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                       : |||: | |||:| |
7 LQGRLQRLLQASGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATRLQKALTEVGNHTTGNL 20
1 MATRLQKALTEVGNHTTGNL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LOGRIORLIOASGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 45.0%;
Matches 9: Concernia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 QGRLLSLLEQSEHRTTGV 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:103185; RXRIP110.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                             BACTERIOPHAGE SPBC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                           RESULT 14
ID 064066
AC 064066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      060811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 15
Q60811
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(MI)	* * * * * *
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 3.36 Seconds 235.385 Million cell updates/sec Fri Aug 20 20:57:47 1999; Run on:

Tabular output not generated.

(1-28) from US08938548B.pep >US-08-938-548B-4 Description: Perfect Score: Title:

196 1 RSGPPGLOGRLORLLOASGNHAAGILTM Seguence:

28

PAM 150 Gap 15 Scoring table:

77977 seqs, 28268293 residues Searched:

0**%** Post-processing:

Minimum Match Listing first

Database:

swiss-prot37 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.486; Variance 47.986; scale 0.656

# SUMMARIES

		dР			COLUMNICO		
Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
П	71	36.2	398	-	VE2_HPV63	REGULATORY PROTEIN E2.	5.54e-01
7	69	35.2	736	7	ALD_MOUSE	ADRENOLEUKODYSTROPHY P	1.20e+00
m	29	34.2	79	Н	NIFU_FRAAL	NIFU PROTEIN.	2.55e+00
4	67	34.2	442	Н	HRDB_STRCO	RNA POLYMERASE PRINCIP	2.55e+00
Ŋ	67	34.2	1477	Н	YOR1_YEAST	OLIGOMYCIN RESISTANCE	2.55e+00
φ	99	33.7	461	Н	VE2_HPV09	REGULATORY PROTEIN E2.	3.69e+00
7	99	33.7	633	-	NODO_RHISB	PROBABLE SULFATE ADENY	3.69e+00
ω	65	33.2	445	Н	RF1M_HUMAN	MITOCHONDRIAL PEPTIDE	5.33e+00
σ	65	33.2	1692	1	CYAA_SCHPO	ADENYLATE CYCLASE (EC	5.33e+00
10	64	32.7	394	٦	RT04_YEAST	MITOCHONDRIAL 40S RIBO	7.66e+00
11	64	32.7	400	Н	ASSY_SYNY3	ARGININOSUCCINATE SYNT	7.66e+00
12	64	32.7	556	٦	YEAJ_ECOLI	HYPOTHETICAL 63.2 KD P	7.66e+00
13	64	32.7	069	П	VTER_EBV	PROBABLE DNA PACKAGING	7.66e+00
14	64	32.7	879	П	YDBH_ECOLI	HYPOTHETICAL 96.8 KD P	7.66e+00
15	63	32.1	199	٦	IL11_MOUSE	INTERLEUKIN-11 PRECURS	1.10e+01
16	63	32.1	248	٦	PSPA_HUMAN	PULMONARY SURFACTANT-A	1.10e+01
17	63	32.1	256	7	YREC_SYNP2	HYPOTHETICAL 28.7 KD P	1.10e+01
18	63	32.1	324	П	ANX3_RAT	ANNEXIN III (LIPOCORTI	1.10e+01
19	63	32.1	429	7	UL88_HCMVA	PROTEIN UL88.	1.10e+01
20	63	32.1	878		ECR_DROME	ECDYSONE RECEPTOR (ECD	1.10e+01
21	63	32.1	972	٦	POLS_IPNVJ	STRUCTURAL POLYPROTEIN	1.10e+01
22	63	32.1	1157	-	PEX1_PICPA	PEROXISOME BIOSYNTHESI	1.10e+01
23	63	32.1	1992	٦	TR12_HUMAN	THYROID RECEPTOR INTER	1.10e+01

1.56e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	3.13e + 01	3.13e + 01	3.13e + 01	3.13e + 01	3.13e+01	3.13e+01	3.13e+01									
TRANSCRIPTIONAL ACTIVA	RETINA SPECIFIC REGULA	THERMOSTABLE CARBOXYPE	SULFITE REDUCTASE (FER	GLYCOPROTEIN B PRECURS	STRUCTURAL POLYPROTEIN	NITRITE REDUCTASE (NAD	KINESIN-LIKE PROTEIN K	KINESIN-LIKE PROTEIN K	FATTY ACID SYNTHASE (E	NEGATIVE FACTOR (F-PRO	PULMONARY SURFACTANT-A	MATING-TYPE LOCUS ALLE	HYPOTHETICAL 57.9 KD P	SERINE/THREONINE PROTE	OROTIDINE 5'-PHOSPHATE	HYPOTHETICAL 34.8 KD P	OUTER MEMBRANE PROTEIN	FACTOR VIII INTRON 22	HYPOTHETICAL 78.9 KD P	ACONITATE HYDRATASE, M	HC-TOXIN SYNTHETASE (E
MT28_YEAST	RGSX_BOVIN	CTAQ_THEAQ	SIR_SYNP7	VGLB_MCMVS	POLS_IPNVN	NIR_NEUCR	KF1A_HUMAN	KF1A_MOUSE	FAS_HUMAN	NEF_HV2NZ	PSPA_PIG	B7_USTMA	YB77_YEAST	AFSK_STRCO	DCOP_MYCTU	YP95_CAEEL	YOPM_YERPE	F812_MOUSE	YCBY_ECOLI	ACON_BOVIN	HTS1_COCCA
-	Н	Н	Н	Н	٦	Н	H	Н	Н	۲-4	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	-
187	374	511	624	928	972	1176	1690	1695	2504	180	249	410	520	799	274	302	367	380	702	780	5217
31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.1	31.1	31.1	31.1	31.1	30.6	30.6	30.6	30.6	30.6	30.6	30.6
62	62	62	62	62	62	62	62	62	62	61	61	61	61	61	9	9	9	9	9	9	9
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

DGAMA K., DELIUS H., MATSUKURA T., KAWASHIMA M., DE VILLIERS E.M.;

"Two novel types of human papillomavirus, HPV 63 and HPV 65:

"Two novel types of human papillomavirus, HPV 63 and HPV 65:

"Two novel types of their clinical and histological features and DNA sequences to other HPV types.";

VIROLOGY 194:789-799(1993).

-! FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-! FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION OF E2RE'S POSITION MITH REGARDS TO PRESSIVE ESCHOOL IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROWITER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSENBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA HUMAN PAPILLOMAVIRUS TYPE 63. VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS. SUBCELLULAR LOCATION: NUCLEAR. SUBUNIT: BINDS DNA AS A DIMER. 01-0CT-1994 (REL. 30, CREATED) 01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE) 15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE) REGULATORY PROTEIN E2. A 398 PRT; STANDARD; SEQUENCE FROM N.A. MEDLINE, 93276568. REPLICATION. RESULT 1 ID VE2\_HPV63 AC Q07850; NAME OF THE PROPERTY OF THE PR

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EMBL, X70828; G312096; -.
PFAM, FR050808; B2\_N; 1.
PFAM, PF00511; E2\_C; 1.
HSSP, P17383; 1DHM.
HSSP, P17383; TANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; UUCLEAR PROTEIN.
SEQUENCE 398 AA, 44550 MW; C99BOGEO CRC32;

Length 398; 36.2%; Score 71; DB 1; I 55.6%; Pred. No. 5.54e-01; Query Match Best Local Similarity ATP (POTENTIAL).
ATP (POTENTIAL).

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661: 661
759 759
179 799
1345 1345
1366 1366
1477 AA; 166727 M
    628
1254
16
295
661
759
799
1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGULATORY PROTEIN E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94265501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
ID VE2_HPV09
AC P36780;
                        NP_BIND
CARBOHYD
                                                                                                                                                                                      SEQUENCE
                                                              CARBOHYD
                                                                                  CARBOHYD
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      UP_BIND
      SETTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VOLCKARET G., VOET M., ROBBEN J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MALI locus reveals 15 complete open reading frames, including 2001, BGL2 and BIO2 genes and an ABC transporter gene.";
YEAST 13:251-259(1997).
-!- FUNCTION: REQUIRED FOR OLIGOMYCIN RESISTANCE.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96069397.

KATZMANN D.J., HALLSTROM T.C., VOET M., WYSOCK W., GOLIN J., VOCKARET G., MOYE-ROWIEX W.S.;

"VECKARET G., MOYE-ROWIEX W.S.;

"Expression of an ATP-binding cassette transporter-encoding gene (YOR1) is required for oligomycin resistance in Saccharomyces cerevisiae.";
                                                                                  ö
                                           Length 442;
                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN; TRANSPORT.
                                                                                                                                                                                                                                                                                                                                               OLIGOMYCIN RESISTANCE ATP-DEPENDENT PERMEASE YOR1
                                         Score 67; DB 1; L
Pred. No. 2.55e+00;
  48413 MW; 4720321F CRC32;
                                                                                                                                                                                                                                                                                 01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                             PRT; 1477 AA.
                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00211; ABC_IRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOL. CELL. BIOL. 15:6875-6883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00005; ABC_trān; 2.
PFAM; PF00064; ABC_membrane; 2.
HSSP: P13569; 1NBD.
ATP-BINDING; FRANSMEMBRANE; GLYC
                                                                                                                     370 LQEQLHSVLDTLSEREAGVVSM 391
                                                                                                                                            | | :|: :|:: ::: ||:::| 7 LQGRLQRLLQASGNHAAGILTM 28
                                       34.2%;
Similarity 31.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z73066; E243252; -.
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE; 97245295.
                                                           Best Local Similarity
    442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; L0003083; YOR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   YOR1 OR YGR281W
                                                                                                                                                                                                                                         YOR1_YEAST
P53049;
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  SEQUENCE
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TRANSMEM
                                         Query Match
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                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELIUS H., HOFMANN B.;

"Primer-directed sequencing of human papillomavirus types.";

CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).

-!- FUNCTION: E2 REGULATES VIABL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESEN

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN PAPILLOMAVIRUS TYPE 9.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P17383; 1DHM.
EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN
GFOHENCE 461 AA; 52141 MW; DA2B4125 CRC32;
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                                                                                                                                                                                                                                                                 Score 67; DB 1; Length 1477;
Pred. No. 2.55e+00;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 461;
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                                                                                                                                                                                                            79B302B8 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-07N-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 AA
POTENTIAL.
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                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSGPPGLQGRLQASGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                     499 GRLQSLLEAPEDDPNQMIEM 518
                                                                                                                                                                                                                                                                                                                                                                                                                  9 GRLQRLLQASGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.7%;
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                 Query Match 34.2%;
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X74464; G397073; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S36593; S36593.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   VAUDIN M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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DAVIS S.C., TZAGOLOFF A., ELLIS S.R.;
"Characterization of a yeast mitochondrial ribosomal protein structurally related to the mammalian 68-kDa high affinity laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; FUNGI; ASCOMYCÒTA; HEMIASCOMYCETES; SACCHAROMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                     LEUCINE-REPEAT; CAMP SYNTHESIS; MAGNESIUM. 999 LEUCINE-RICH REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 1; Le
Pred. No. 5.33e+00;
3; Mismatches 3:
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01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATI
MITOCHONDRIAL 40S RIBOSOMAL PROTEIN MRP4.
MRP4 OR YHLO04W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIRR 3.
LIRR 4.
LIRR 5.
LIRR 6.
LIRR 7.
LIRR 9.
LIRR 10.
LIRR 11.
LIRR 11.
LIRR 12.
LIRR 14.
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LIRR 17.
LIRR 19.
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LIRR 21.

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J. BIOL. CHEM. 267:5508-5514(1992).
                                                                                                                                                                                           EMBL; M26699; G173339; -.
EMBL; M24942; G173379; -.
EMBL; AL023859; E1298611; -.
PIR; A33988; A33988.
PIR; A3539; A33539;
PPAM; PPF00481; guanylate_cyc; 1.
PPAM; PF00560; LRR; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190333 MW;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RT04_YEAST
P32902;
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LYASE;
DOMAIN
REPEAT
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REPEAT
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REPEAT
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMUBA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.
SHINDO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                        ij
STRAIN=S288G / AB972;
MEDLINE; 94378003.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
JOHNSTON M., ANDREWS S., BRINKMAN R., GEISEL C., KIRSTEN J.,
KUCKBA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
LATREILLE P., LOUIS B.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.
WIRNAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
VIGNAIL D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                           RIBOSOME.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOMATION UPDATE)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: COMPONENT OF THE SMALL SUBUNIT OF MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 1; Le
Pred. No. 7.66e+00;
1; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA; 44151 MW; 5226C1B0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M82841; G171982; --
EMBL; U10555; G500819; --
PIR; S47429; S27429; SGD; L0001154; M42115; SGD; L0001154; MRP4.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
PROMISE; PS009618; S2; 1.
RIBOSOMAL PROTEIN; MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNECHOCYSTIS SP. (STRAIN PCC 6803).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%;
larity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                 SCIENCE 265:2077-2082(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 RAGQRGLQNRLAR 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSGPPGLQGRLQR 13
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P77973;
01-NOV-1997 (REL.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                       AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOYO K., INDAA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAH H., KASHIMOTO K., KIM S., KIMMEA S., KITAGAWA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., NAKAMURO H., NISHIO Y., OSHIMA T., SATIO N., SAMPEI G., SEKI Y., TAGAMI H., TAKENOTO K., WADA C., YAMANOTO Y., YANO M.; SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97070356.

MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;

"Molecular cloning and characterization of murine interleukin-11.";

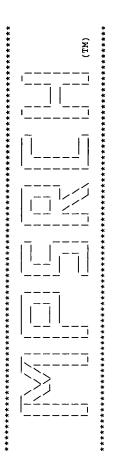
EXP. HEMATOL. 24:1369-1376(1996).

-i. FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,

T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                  MEDLINE; 9742617.

BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., BLATTNER F.R., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLARK D.P.;
                                                                                                                                    MAU B., SHAO Y.;
"The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 1; Length 879;
Pred. No. 7.66e+00;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARI
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 36 I -> L (IN REF. 3).
879 AA; 96834 MW; 8BFD7CF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000235; G1787646; -.
EMBL; D90776; G1742260; -.
EMBL; D90777; G174224; -.
EMBL; U36928; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 GVDGRLQAILQAHENELGDFVLHM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ::|||| :||| | : :| | 6 GLOGRLORLLOASGNHAAG-ILLTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 32.78;
Local Similarity 45.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-331 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOGENE; EG13180; YDBH. HYPOTHETICAL PROTEIN.
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   STRAIN=K12 / MG1655;
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IL11_MOUSE
P47873;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
CELLS AND SYNERGIZES WITH IL-3 IN SUPPORTING MURINE MEGARARYOCYTE COLONY FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 1; LA
Pred. No. 1.10e+01;
4; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
INTERLEUKIN-11.
; 1CB30772 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: Fri Aug 20 20:57:57 1999 Job time : 10 secs.
                                                                                                                                                                                                                                                                                                                               MGD; MGI:107613; IL11.
CYTOKINE; GROWTH FACTOR; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                   199 IN
21522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 ALQARLERLLR 138
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6 GLQGRLQRLLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 199 AA;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 20:57:08 1999; MasPar time 4.89 Seconds 229.521 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-4 (-128) from US08938548B.pep 196 1 RSGPPGLQGRLQARLOASGNHAAGILIM 28

Description: Perfect Score: Seguence:

PAM 150 Gap 15 Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 30.618; Variance 52.462; scale 0.584 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		φ,					
Result No.	Score	Query Match	Query Match Length	DB	Ð	Description	Pred. No.
1	71	36.2	511	. 7	T02269	hypothetical protein	1.60e+00
7		35.2	439		561858		3.24e+00
m	69	35.2	736	7	S47044	, G	3.24e+00
4		34.7	178		E69913	pro	4.58e+00
5	49	34.2	145		T00987		6.46e+00
9	67	34.2	442		S11712	- 54	6.46e+00
7	67	34.2	510		S41307	transcription initiat	6.46e+00
∞	67	34.2	525		JN0443	٠.	6.46e+00
თ	67	34.2	528	7	JN0445	transcription initiat	6.46e+00
10	67	34.2	1420		T02644	probable ABC transpor	6.46e+00
11	29	34.2	1477		S64616	YOR1 protein - yeast	6.46e+00
12	67	34.2	2115	7	S23647	ı	6.46e+00
13	99	33.7	461		S36593	걸	9.07e+00
14	65	33.2	178	7	S26481	calcium-binding prote	1.27e+01
15	65	33.2	1692	•	A33988	adenylate cyclase (EC	1.27e+01
16	64	32.7	263	•	S51155	hypothetical protein	1.77e+01
17	64	32.7	325		QQBE38	BGRF1 protein - human	1.77e+01
18	64	32.7	394	7	A42115	ribosomal protein S2,	1.77e+01
19	64	32.7	400		S76929	hypothetical protein	1.77e+01
20	64	32.7	532		A46101	protein-tyrosine-phos	1.77e+01
21	64	32.7	548		B46101	protein-tyrosine-phos	1.77e+01
22	64	32.7	556		B64939	hypothetical protein	1.77e+01
23	64	32.7	879	7	H64888	membrane protein ydbH	1.77e+01

,		102269 #type complete	#ty	69	T02269	Н	RESULT ENTRY
		ALIGNMENTS					
3.41e+01	fatty-acid synthase (	G01880	7	2509	31.6	62	45
3.41e+01		A57788	Н	2504	31.6	62	44
3.41e+01	glycoprotein B precur	VGBEMC	Н	928	31.6	62	43
3.41e+01	probable helicase pro	G71081	7	526	31.6	62	42
3.41e+01	carboxypeptidase (EC	JC2294	~	511	31.6	62	41
3.41e+01	N-hydroxyarylamine O-	B64899	7	281	31.6	62	40
3.41e+01	transcription factor	S48361	7	187	31.6	62	39
3.41e+01	deoxyuridine 5-tripho	D69081	7	150	31.6	62	38
3.41e+01	allergen TBA-1 - Toxo	B49139	~	36	31.6	62	37
2.46e+01	probable cobN protein	E70940	~	1194	32.1	63	36
2.46e+01	PAS1 protein - yeast	A55152	7	1157	32.1	63	35
2.46e+01	genome polyprotein -	GNXSIV	Н	972	32.1	63	34
2.46e+01	ecdysone receptor - f	A41055	7	878	32.1	63	33
2.46e+01		S09852	7	429	32.1	63	32
2.46e+01	Н	S76765	7	331	32.1	63	31
2.46e+01	•	LURT3	Н	324	32.1	63	30
2.46e+01	hypothetical protein	Q3YCRQ	Н	256	32.1	63	29
2.46e+01	pulmonary surfactant	LNHUP1	-	248	32.1	63	28
2.46e + 01	pulmonary surfactant	LNHUP6	Н	248	32.1	9	27
2.46e+01	pulmonary surfactant	LNHUPS	Н	248	32.1	63	56
2.46e+01	pulmonary surfactant-	151921	~	248	32.1	63	25
1.77e+01	mitogen-activated pro	JE0363	m	1288	32.7	64	24

-1	T02269 #type complete	Afound Industrial protein Tibble - Arabidopsis Chailana #formal_name Arabidopsis thaliana #common_name mouse-ear	oress 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Mar-1999	TO		G.; Oji, O.; Liu, S.; Li, J.; Araujo, R.; Au, M.; Brendel, V.; Buehler, E.; Conwav, A.B.; Conwav, A.R.; Dewar, K.;	Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn,	P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.A.;	Theologis, A.		iption Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.		tatus preliminary; translated from GB/EMBL/DDBJ	##molecule_type DNA	esidues 1-511 ##label VYS	##cross-references EMBL:AC004473; NID:q3108025; PID:q3249066		osition 1	ns 27/3; 48/3; 392/2; 416/1; 452/2; 477/3	T13D8.6	#length 511 #molecular-weight 55547 #checksum 7824	יים יידי יידי יידי יידי יידי יידי יידי	
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	ENTRY	ORGANISM	DATE	ACCESSIONS	#authors	•				#submission	#description	#accession	##status	##molecr	##residues	##CIOSS-	GENETICS	#map_position 1	#introns	#note	SUMMARY	Outre Watch	

Score 71; DB 2; Length 511; Pred. No. 1.60e+00; 4; Mismatches 7; Indels 36.2%; Query Match Best Local Similarity 52.2%; Matches 12; Conservative

; 0

Gaps

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308 QSTPPGLQARAGRLVAAKSTLAA 330 23 : | | | | | | | : | : | | | RSGPPGLQGRLQRLLQASGNHAA 쉱 ò

TITLE ORGANISM DATE RESULT ENTRY

S61858 #type complete
hrpE protein - Pseudomonas solanacearum
#formal\_name Pseudomonas solanacearum
20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change
17-Mar-1999
S61888
S61846 ACCESSIONS REFERENCE #authors

van Gijsegem, F.; Gough, C.; Zischek, C.; Niqueux, E.; Arlat, M.; Genin, S.; Barberis, P.; German, S.; Castello, P.;

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*start_codon
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                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Shiina, T.; Tanaka, K.; Takahashi, H.
#journal Gene (1991) 107:145-148
#title Sequence of hrdb, an essential gene encoding sigma-like transcription factor of Streptomyces coelicolor A3(2): homology to principal sigma factors.
#cross_references_MUID:92077425
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is protein is the functional homolog of the principal sigma factors involved in the transcription of housekeeping genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sigma-like transcription factor
#formal_name Streptomyces coelicolor
03-May-1994 #sequence_revision 20-Feb-1995 #text_change
29-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A40116
Tanaka, K.; Shiina, T.; Takahashi, H.
Science (1988) 242:1040-1042
Multiple principal sigma factor homologs in eubacteria:
identification of the "rpob box".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jo
submitted to the EMBL Data Library, April 1998
Arabidopsis thaliana chromosome II BAC T9J22 genomic
                                                                                                                                                                                                              #length 145 #molecular-weight 15355 #checksum 3045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka, K.; Shiina, T.; Takahashi, H.
submitted to the EMBL Data Library, May 1990
Multiple homolog genes for principal sigma subunit
Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; nucleic acid sequence not shown; compared with conceptual translation
                                                                                                    ##residues 1-145 ##label ROU ##cross-references EMBL:AC002505; NID:q2739359; PID:q2739379
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                                                                    preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
##residues 1-442 ##label EMB
##cross-references EMBL:X52983; NID:g48744; PID:g48745
##experimental_source strain A3(2)
                                                                                                                                                                                                                                                Score 67; DB 2; LA Pred. No. 6.46e+00;
                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237-288 ##label TAN
                                                                                                                                                      #map_position II
#introns 17/1; 49/3; 78/2; 123/2
#note T9J22.21
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                                                                                                                                                                                                                                                                                                                                        5 PGLQGRLQRLLQASGNHAAG 24
                                                                                                                                                                                                                                                Query Match 34.2%;
Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                  Conservative
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                                     sequence.
T00987
                                                                                      ##molecule_type_DNA
##residues 1-1
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Marcos, A.T.; Diez, B.; Gutierrez, S.; Fernandez, F.J.; Velasco, J.; Martin, J.F. submitted to the EMBL Data Library, December 1993 organization and expression of the hrdB-sprC gene cluster of streptomyces griseus encoding a signa factor protein and a serine protease. Role on growth and sporulation of
                                                                                                                                                                                                                                                                                                                                                                                                                  S41307 #type complete transcription initiation factor sigma - Streptomyces griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *superfamily Streptomyces transcription initiation factor sigma; transcription initiation factor sigma katF homology DNA binding; sigma factor; transcription initiation
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#journal Gene (1992) 122:63-70
#title Four genes in Streptomyces aureofaciens containing a domain characterstic of principal sigma factors.
#cross-references MUID:93083996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces aureofaciens
#formal_name Streptomyces aureofaciens
30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change
17-Mar-1999
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Streptomyces griseus
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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                                                  #domain transcription initiation factor sigma katF
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#length 510 #molecular-weight 55795 #checksum 1415
                                                                       homology #label KTF
#length 442 #molecular-weight 48413 #checksum 4794
DNA binding; sigma factor; transcription initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JNO443 #type complete transcription initiation factor sigma homolog hrdB
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##cross-references EMBL:X75952; NID:g440164; PID:g581664
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Pred. No. 6.46e+00;
11; Mismatches 4; Indels
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##molecule_type DNA
##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:g153306; PID:g153306
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Pred. No. 6.46e+00;
11; Mismatches 4;
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Best Local Similarity 31.8%;
Matches 7; Conservative
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Local Similarity 31.8%;
nes 7; Conservative
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S41307
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##residues 1-2115 ##label YAN
##cross-references EMBL:211583; NID:935118; PID:935119
##cross-references EMBL:211583; NID:935118; PID:935119
##note the authors translated the codon GAG for residue 781 as
G1y, TTC for residue 1775 as Pro, and GGA for residue
2067 as G1u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuan, R.S.; Fitzpatrick, D. submitted to the EMBL Data Library, September 1990 Structural analysis of mouse placental 57-KD Calcium-binding
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                                                                                                       Yang, C.H.; Lambie, E.J.; Snyder, M.
J. Cell Biol. (1992) 116:1303-1317
NuMA: an unusually long coiled-coil related protein in the
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submitted to the EMBL Data Library, August 1993
Primer-directed sequencing of human papillomavirus types.
336593
   #formal_name Homo sapiens #common_name man
19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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#formal_name human papillomavirus type 9
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                        #molecular-weight 238273 #checksum 439
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6; Mismatches 10; Indels
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Pred. No. 6.46e+00;
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NuMA protein - human
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Paccession S23647
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Best Local Similarity 38.5%;
Matches 10; Conservative
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Best Local Similarity 52.9%;
Matches 9; Conservative
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##cross-references GB:M24942; NID:g173378; PID:g173379
##note the authors translated the codon TGC for residue 626 as Ser, and GCC for residue 1243 as Gly
FICATION #superfamily leucine-rich alpha-2-glycoprotein repeat homology; yeast adenylate cyclase catalytic domain homology
DS phosphorus-oxygen lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7989-7993
#title The adenylyl cyclase gene from Schizosaccharomyces pombe.
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0
                                                    calcium binding
#length 178 #molecular-weight 19960 #checksum
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adenylate cyclase (EC 4.6.1.1) - fission yeast
(Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
23.Mar-1990 #sequence_revision 23-Mar-1990 #tex
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                                                                                                                        33.2%; Score 65; DB 2; Length 178. 30.8%; Pred. No. 1.27e+01; vative. 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young, D.; Riggs, M.; Field, J.; Vojtek, A.;
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Pred. No. 1.27e+01;
3; Mismatches 3; Indels
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##residues 1-178 ##label TUA
##cross-references EMBL:X56603; NID:q53597; PID:q53598
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#length 1692 #molecular-weight 190332
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| RSGPPGLQGRLQRLLQASGNHAAGIL 26
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Similarity 57.1%;
8; Conservative
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##residues 1-1
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MPsrch\_pp protein, - protein database search, using Smith-Waterman algorithm

Fri Aug 20 20:59:00 1999; MasPar time 1.72 Seconds 165.470 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-4 (1-28) from US08938548B.pep 196 1 RSGPPGLQGRLQRLLQASGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

106580 segs, 10152877 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Mean 20.494; Variance 80.948; scale 0.253 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No.	Score	Query Match	Length	DB	QI	Description	Pred. No.
П	68	34.7	716	່ຕ	PCT-US95-1	Sequence 4, Applicatio	2.13e+01
7	29	34.2	442	7	US-08-363-	4, 4	2.59e+01
m	67	34.2	442	7	US-08-363-	11,	2.59e+01
4	67	34.2	445	7	US-08-363-	12,	2.59e+01
Ŋ	67	34.2	445	7	US-08-363-	'n	2.59e+01
φ	67	34.2	1841	~	US-08-804-	9	2.59e+01
7	99	33.7	10	٣	PCT-US91-0	'n	3.14e+01
ω	65	33.2	381	7	us-08-858-	'n	3.81e+01
σ	65		381	N	US-08-858-	1,	3.81e+01
10	62	31.6	176	٣	PCT-US96-1	9	6.78e+01
11	62	31.6		~	us-08-659-	ý	6.78e+01
12	62	31.6		Н	US-08-469-	10,	6.78e+01
13	9	30.6		Н	US-07-941-	7	9.
14	9	30.6		-	US-08-792-	ω̈́	9.90e+01
15	9	30.6		Н	US-07-949-	4	ģ
16	9	30.6		~	US-08-814-	4	9.90e+01
17	9	30.6		Н	US-08-115-	7	9.90e+01
18	9	30.6		Н	US-08-017-	4	9.90e+01
13	9	30.6		m	PCT-US93-0	7	9.90e+01
20	9	30.6		Н	US-07-745-	14,	9.90e+01
	9	30.6		Н	US-08-115-	4, 4	9.90e+01
22	9	30.6	296	H	US-07-941-	4,	9.90e+01
23	9	30.6	296	Н	US-08-165-	Sequence 14, Applicati	9.90e+01

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e 14, Application 14, Application 2, Application 214, Application 214, Application 2, Application 3, Application 3, Application 2, Applicatio	AA.		-INTERACTING LATED MOLECULES 00 ion #1.30
Sequenc Seq Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc Se	S RT; 716	11	RECEPTOR S AND RE P.C. Suite 31 16311 2
US-07-921- PCT-US93-0 PCT-US93-0 US-08-363-1 US-08-363-0 US-08-363-0 US-08-363-0 US-08-363-0 US-08-363-0 US-08-444-0 US-08-446-0 US-08-646-0	ALIGNMENT STANDARD; P	PC/TUS95163:	id distribution of the control of th
2296 3 3 2 2 9 6 8 3 3 2 2 9 6 8 3 3 2 2 9 6 8 3 3 2 2 9 6 8 3 3 2 2 9 6 8 3 3 2 2 9 6 8 3 3 2 2 9 6 8 3 2 9 7 1 1 2 2 1 1 1 2 2 1 1 1 1 2 2 1 1 1 1	-4 STAN	ication	Sequence 4, Application PC/TUS9 GENERAL INFORMATION: APPLICANT: Moore, David APPLICANT: Seol, Wongi APPLICANT: Chol, Hueng-Sik TITLE OF INVENTION: POLYPEP NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richard STREET: 225 Franklin Stre CITY: Boston STATE: MA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER READABLE PRESIES SOFTWARE: PatentIn Releas CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/U FILING DATE: 13-JAN-1995 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,1 REGISTRATION NUMBER: 30,1 REGISTRATION NUMBER: 30,1 REFERENCE/DOCKET NUMBER: TELEPHONE: 617/542-8906 TELEPHONE: 617/542-8906 TELEFANK: 617/542-8906 TELEFANK: 617/542-800 TELEFANK: 617/542-8006 TELEFANK: 617/542-8006 TELEFANK: 617/542-8006 TELEFANK: 716 amino acids
222950000000000000000000000000000000000	95-16311·	ce 4, Appl:	GENERAL INFORMATION APPLICANT: MOOFE, APPLICANT: MOOFE, APPLICANT: Seel, APPLICANT: Seel, APPLICANT: Choi, TITLE OF INVENTION UNMBER OF SEQUENCE CORRESPONDENCE ADI ADDRESSEE: Fish STARET: AS FREET: AS FREET: BA COUNTRY: BOSTON STARET: MA COUNTRY: BAS INFORMATION STARET: MA COMPUTER: BAD COMPUTER: IBM FOR COMPUTER: BAPLICATION NUM FILING DATE: 13 APPLICATION NUM FILING DATE: 13 ATTORNEY/AGENT IN NAME: CLARK, PR REGISTRATION NUM FELEFRAN: 617/54 TELEFRAN: 617/54 TELE
42000000000000000000000000000000000000	RESULT 1 ID PCT-USS	xxxxx	Sequel GENERAL APPLICATION NUTTHEN APPLICATION
	RES ID	SX CX C	\$8888888888888888888888888888888888888

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FITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
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                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,255

FILING DATE: 23-DEC-1994

CLASSIFICATION: 435

ATONNEY/AGENT INFORMATION:

NAME: MONROY, GLADYS 32,430

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 32,430

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: (415) 813-5600

TELEFRAX: (415) 494-0792
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Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHOff, Bradley S.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1841 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
NCE 445 AA; 48583 MW; 967304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08804227C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 445 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :|: :|: :: ||:::| 7 LQGRLQRLLQASGNHAAGILIM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                   NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 46285.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.2%;
Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
ID US-08-804-227C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                 APPLICANT: JACOBS, Jr., WILLIAM R.
APPLICANT: BLOOM, BARRY R.
APPLICANT: COLLINS, DESMOND M.
APPLICANT: CLISLE, GEOFFREY W.
APPLICANT: FASCOPELLA, LISA
APPLICANT: KAWAKAMI, RIKU P.
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08363255
Patent No. 5783386
GENERAL INFORMATION:
APPLICANT: BLOOM, BARRY R.
APPLICANT: BLOOM, BARRY R.
APPLICANT: COLLINS, DESMOND M.
APPLICANT: de LISLE, GEDFFREY W.
APPLICANT: ASCOPELLA, LISA
APPLICANT: RAWAKAMI, RIKU P.
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
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CURRENT APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTOCNEY AGGNT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
ICE 445 AA; 48583 MW; 967304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORKSTER
STREET: 755 Page Mill Road
               Sequence 12, Application US/08363255
Patent No. 5783386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08363255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 25.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 494-0792
TELEEX: 706141
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 LQEQLHSVLDTLSEREAGVVSM 394
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| LQGRLQRLLQASGNHAAGILTM 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                  Abure.
STREET: 755 ...
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
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LOCATION: 1..176
OTHER INFORMATION: /note= "rev protein encoded by HIV-2KR"
NCE 176 AA; 19639 MW; 145168 CN;
                                                                                                       Sequence 6, Application PC/TUS9611445
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: ISOlation of Novel HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STRRET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUMTRY: USA
ZIF: 9012-2628
                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US96/11445 FILING DATE: CLASSIFCATION: ATTORNEY/ACE...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 3; Length 176;
Pred. No. 6.78e+01;
5; Mismatches 9; Indels
 176 AA
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                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET WUMBER: 5555-399C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEPHONE: (213) 977-1001
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                  Sequence 6, Application PC/TUS9611445
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Patent No. 5883081
GENERAL INFORMATION:
APPLICANT: Kraus, Guenter
APPLICANT: Wong-Staal, Flossie
APPLICANT: Talbott, Randv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08659251
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSGPPGLOGRLORLLOASGNHAAGI 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 176 amino acids TYPE: amino acid STRANDEDNESS:
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.0%;
Matches, 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
PCT-US96-11445-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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US-08-659-251-6
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                                                                                                                                                                                                    Sequence 1, Application US/08858052
Patent No. 5849498
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTYRUL-COENZYME A
TITLE OF INVENTION: HURADASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inoyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 3.81e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/858,052
                                                                                              381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0294 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA; 42808 MW; 739653 CN;
                                                                                              PRT;
          296 KMSPTSLKITLRQLMEGSSKTLQEVLTM 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                             Seguence 1, Application US/08858052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity 28.6%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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LIBRARY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
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Gaps

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SEQUENCE

RESULT

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Search completed: Fri Aug 20 20:59:08 1999 Job time: 8 secs.
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                            Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
             Protein
                     1..178
                                       NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                  129 LQARLDRLLR 138
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                                                                                                                                   7 LOGRIQRILO 16
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           NAME/KEY:
LOCATION:
FEATURE:
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US-07-949-516A-4
                                                 LOCATION:
  FEATURE:
                                                          SEQUENCE
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Pred. No. 9.90e+01;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APLICANT: TILLE OF INVENTION: 116
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902
                                                                                                                                                                                                                                                                                                          199
                                                                        NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: INDUSI
TELECOMMUNICATION INFORMATION:
TELEPRAN: (215) 540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08792019B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INC.

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-4

FFORMATION FOR SEQ ID NO: 8:
                                              FILING DATE: 19920902
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                           Query Match 30.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                               AMINO ACID
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7 LQGRLQRLLQ 16
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                                                                                                                                                                                                                                                                                                LT 14
US-08-792-019B-8
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Pred. No. 9.90e+01;
3; Mismatches 0; Indels
                                                        Score 60; DB 1; Length 199;
Pred. No. 9.90e+01;
                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/07949516A
Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: No.
CITY: USA
COUNTRY: USA
CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19-NOV-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                    199 AA
                                                                                                  3; Mismatches
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JENCE 199 AA; 21429 MW; 188641 CN;
TION: -21..0
199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATORNEY, AGENT TREPRATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: 5174!
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acids
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<b>水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水水</b>	    	**************************************
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 20:56:23 1999; MasPar time 4.60 Seconds 129.426 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-4 (1-28) from US08938548B.pep Title:

1 RSGPPGLQGRLQRLLQASGNHAAGILTM 28 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 20:part10 11:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 22.064; Variance 88.246; scale 0.250

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

			Pred. No.		epto 7.83e-11	epto 3.06e-10	35. 3.06e-10	٣	or 3	or i 6.30e+01	ur2R 7.60e+01	_	e OR 7.60e+01	7	on p 7.60e+01	zuel 7.60e+01	(2). 9.16e+01	4	1	1-10 1.60e+02
	·		Description		Human HFGAN72 recepto	Mouse HFGAN72 recepto	Mouse hypocretin 35	Rat hypocretin 35.	Rat HFGAN72 receptor	Retinoid X receptor	S. cerevisiae scaur2R	Saccharomyces cerevis	Tylactone synthase OR	LexA/NuMA fusion prot	GAL4/HA/NuMA fusion	Streptomyces venezuel	"p33" N-terminal (2)	Human 3-hydroxyisobut	New polypeptide based	Vector PSP 35K-1A-10
SOFTERNIES			П		W61381	W61383	W50158	W50157	W61382	R99737	R67691	W10424	W22605	W21732	W21731	W19629	R20235	W81135	R00579	R05091
			DB	:	33	33	30	30	33	18	13	22	56	23	23	23	4	38	Н	~
			Match Length DB		131	123	130	130	130	716	1477	1477	1841	2192	2272	4630	10	381	32	248
	æ	Query	Match		100.0	6.96	6.96	96.9	6.96	34.7	34.2	34.2	34.2	34.2	34.2	34.2	33.7	33.2	32.1	32.1
			Score		196	190	190	190	190	89	67	67	67	67	67	49	99	65	63	63
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		ry)	ry)	first entry	١	-19		255
		131 AA.	'n;	Protein;	standard;		RESULT 1 ID W61381	題の数
		ALIGNMENTS						
2.75e+02	Platenolide synthase	7	26	3724	o.	9	45	
.75e+0	Human KM-102-derived	4	38	551	0	9	44	
۲.	e-assoc	8 6		530		09	. <b>4</b> .	
2.75e+02 2.75e+02	Human interleukin-ii A himan mitant alanin	W02202 W46904	2 5	495	30.6	9 0	4 7 7 7	
.92e+0	Protein (OA-519) cros	W32881		2509	;,	62	0,	
	Thermus aquaticus hea	R49835		510	i.	62	39	
1.92e+02	0	W13056	23	176	ij	62	38	
•	Ecdysone receptor.	K13/93		8/8	'nς	500	30	
•	DHR23alpha protein.	R32889	9	878	ď.	63	35	
•	ecdysone r	W33655	28	746	ď	63	34	
1.60e+02	มูน	W33654	2 8	746	. ·	9 6	9 M	
.60e+0	receptor	W45513	5 6	550	oi o	63	31	
•	X ASP encode	R04217	Н	271	ς.	63	30	
.60e+0	2K alveolar	R04212	Н	271	ď	63	29	
1.60e+02		P60661	n	271		93	, 8 7 8	
	Sequence of human alv	P60665	יז רי	248	'n c	200	270	
1.60e+02	sedneuce c	P60666	m	248	ri.	63	25	
1.60e+02	nonary su	P70662	7	248	3	63	24	
60e+0	oza Asr nce dedu	P80694	-	248	, N	93	3.6	
1.60e+02	35kd pulmonary surfac	P70663	~ ~	248	, c	9	77	
.60e+0	edneuce dednce	P82980	Н,	248	oi.	63	20	
60e+0	Human 32K ASP encoded	R04215	٦	248	ς.	63	19	
1.50e+02		*	m	248	ď	63	18	
,,,,,,	Plasmid pASPcg-SV(10)	560442			;	3		

PR 26-SEP-1995; US-939093.

PR 17-DEC-1996; US-939093.

PR 17-DEC-1996; US-82019.

PR 17-DEC-1996; US-82019.

PR 02-JUL-1997; US-82019.

PA (SMIK ) SMITHKLINE BEECHAM FOLC.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

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PA (SMIKH ) SMIKHLINE BEECHAM PLC.

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PA (SMIKHLINE BEE Human Heard's receptor procein.
Heard receptor; eating disorders; renal disease; heart failure;
Sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder. 34..66 /note= "Ligand 72A" 70..97 /note= "Ligand 72B" Location/Qualifiers 17-DEC-1997; 310216 Homo sapiens EP-849361-A2 Region Region 

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R99737
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Claim 5: Fig 4: 35pp: English.

Cused for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired classes tolerance and sexual dysfunction. The agonist is useful for treating and cachexia. The HFGAN72 receptor infections, particularly infections cachexia. The HFGAN72 receptor cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, cancers, myocardial infarction, ulcers, asthma, allergies, benign pectoris, myocardial infarction, ulcers, asthma, allergies, benign constatic hypertrophy, chronic renal failure, renal disease, impaired constant caches and neurological discases as the constant constant caches and neurological discase.
                                                                                                                                                                                                                                                                                                                                                                         Rat HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure; sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention; osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington' disease or Gilles dela Tourett's syndrome.
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor.
                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 96.9%; Score 190; DB 33; Length 130; Best Local Similarity 92.9%; Pred. No. 3.06e-10; Matches 26; Conservative 2; Mismatches 0; Indels
                                                                                                                                               DB 30; Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFGAN72 receptor ligands - and corresponding DNA, agonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 190; Dec. 100: Pred. No. 3.06e-10;
                                                                                                                                                                                0; Indels
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                                                                                                                                            Score 190; DB 30; Pred. No. 3.06e-10;
                                                                                                                                                                                2; Mismatches
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/note= "Ligand 72A"
69..96
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                                                                                                                                                                                                                                                                                                                        standard; Protein; 130
                                                                                                                                             96.98;
92.98;
                                                                                                                                                              Best_Local Similarity 92.9%;
Matches 26; Conservative
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17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological disorder.
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                                                                                                         130 AA;
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17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
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W61382
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                                                                                                                                                                                                                                                                                                      Retinoid X receptor (RXR) interacting protein (RIP) - useful to modulate or mediate RXR function, anti-RIP antibodies can be used to determine RIP subcellular distribution patterns

Claim 2, Page 48-50, 90pp; English.

Mouse retinoid X receptor (RXR) interacting protein RIP110 (R99737) is a candidate transcriptional co-activator. It was identified using an in vivo interaction trap system for the isolation of proteins that physically interact with RXRs, esp. with the ligand binding domain of human RXR alpha. Recombinant RIP110 can be obtd. using a cDNA clone (T31930) obtd. from a mouse liver library. RIPS (see also R99735-36 and R99738-39) can be used to modulate or mediate RXR function, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 77-84; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scaurlR (Q75954) was isolated from 1 library, and resistant gene scaurlR (Q75956) from the other. A DNA fragment of scaurl was used as a probe to isolate a sensitive gene, scaurlS (Q75955), from the sensitive strain. A TB52A mutation leading to a F158Y conversion gave rise to the resistance of scaurlR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as
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Pred. No. 7.60e+01;
6; Mismatches 6; Indels (
                                                           Retinoid X receptor interacting protein RIP110.
Retinoid X receptor interacting protein; RXR; RIP; RIP110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may be used therapeutically or to raise antibodies.
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Pred. No. 6.30e+01;
6; Mismatches 4;
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S. cerevisiae scaur2R gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R67691 standard; Protein; 1477 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Takesako K;
standard; Protein; 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%;
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Best Local Similarity 44.4%;
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08-DEC-1995; U16311.
13-JAN-1995; US-372652.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                              Choi H, Moore D, Seol W;
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WPI; 95-023286/04.
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                                                                                                         Mus sp.
WO9621677-A1
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Gaps ö

> 69 rpgppglqgrlqrllqangnhaagiltm 96

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Expression cassettes for production of polyhydroxyalkanoate(s) provide wide range of biodegradable polymers for medical or
   WPI; 97-341701/31.
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                                                   industrial use
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                              Language 28-36; 78pp; English.

The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for detect NIP (or their complexes) and to block their activity for which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by
                                                                                             01-OCT-1997 (first entry)
GAL4/HA/NuMA fusion protein.
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding nuclear mitotic appts, interacting proteins - useful for modulating cell division and proliferation and
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Pred. No. 7.60e+01;
5; Mismatches 3; Indels (
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Streptomyces venezuelae polyketide synthase.
Polyketide synthase; polyhydroxyalkanoate monomer synthase; polyhydroxybutyrate; biodegradable polymer; vep gene; metabolic engineering.
Streptomyces venezuelae.
W09722711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   administration of the appropriate functional protein.
                                                                                                                                                                                                                                   /label= Residues_18-2116_of_NuMA
365..1864
                                                                                                                                                                                             /label= GAL4_DNA_binding_domain
148..174
                                                                                                                                                                                                                     /label= Hemaglutinin_epitope 175..2272
                                                                                                                                                                                                                                                                     /label= Coiled_coil_region
                                                                                                                                                                       Location/Qualifiers
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W19629 standard; Protein; 4630 AA.
W19629;
                                                                     W21731
W21731;
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18-DEC-1995; U20119.
19-DEC-1995; US-008847.
(MINU) UNIV MINNESOTA.
Sherman DH, Williams MD, Xue Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
838 ragrkglearlqqlgea 854
                                                                                                                                                                                                                                                                                                                                            McPherson SMG, Snyder MP;
WPI; 97-077270/07.
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                |:| ||::|||:|
1 RSGPPGLQGRLQRLLQA 17
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| RSGPPGLQGRLQRLLQA 17
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07-JUN-1996; U09504.
07-JUN-1995; US-478408.
(UYXA.) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2272 AA;
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                                                                                                                                                            Homo sapiens
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Claim 55; Fig 23; 91pp; English.

Claim 55; Fig 23; 91pp; English.

Claim 55; Fig 23; 91pp; English.

Claim 55; Play 57; Pla
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A protein, designated p33, is found on the surface of several types of lymphocyte cells, including OKT3-stimulated primary T-cells, antigen-specific IL-2 dependent CTL clones, and a PMA-stimulated human T-cell hybridoma, IL-23.D7. It forms a novel complex with lymphotoxin (LT). The N-terminal of the p33 protein contains the sequence represented in R20234 or R20235. The sequence at the 6th cycle appeared to be a mixt. of both G and L indicating possible polymorphism. The p33 protein may have one of these sequences or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 7.60e+01;
...amatches 7; Indels
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Pred. No. 9.16e+01;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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W81135 standard; Protein; 381 AA.
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Best Local Similarity 33.3%;
Matches 8; Conservative
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(REGC ) UNIV OF CALIFORNIA.
Browning J, Ware CF;
WPI; 92-041521/05.
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Similarity 88.9%;
8; Conservative
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27-JUN-1991; U04588.
27-JUN-1990; US-544862.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 7.71 Seconds 358.518 Million cell updates/sec Fri Aug 20 21:00:11 1999; Run on:

Tabular output not generated.

Title:

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL.......GRRCPTATATALAPRGGSRV 130 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseg35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part19 20:part16 16:part16 17:part11 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38 Database:

Mean 30.024; Variance 131.695; scale 0.228 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	0,000	& Query	8 Query Match Ionath DB	2		***	,
1000		Marcii	reng cu	3 :	TD	Description	Pred. No.
954	<+	100.0	130	30	W50157	Rat hypocretin 35.	5.23e-79
954	₹*	100.0	130	33	W61382	Rat HFGAN72 receptor	5.23e-79
891	Н	93.4	130	30	W50158	Mouse hypocretin 35.	6.08e-73
85	ო	89.4	123	33	W61383	Mouse HFGAN72 recepto	2.73e-69
78	2	82.0	131	33	W61381	Human HFGAN72 recepto	1.76e-62
Ξ	m	11.8	378	39	W84185	Glial cell line-deriv	4.63e-01
7	m	11.8	400	39	W84186	Glial cell line-deriv	4.63e-01
Ξ	m	11.8	400	33	W84180	A GDNFR-alpha-related	4.63e-01
Ξ	m	11.8	400	32	W65116	Human GDNF alpha-3 re	4.63e-01
Ξ	m	11.8	400	32	W65117	Human GDNF alpha-3 re	4.63e-01
H	13	11.8	400	28	W37463	Human Ret ligand RetL	4.63e-01
•	96	10.1	556	58	W27598	Human fibulin type 1	9.01e+00
•	96	10.1	266	~	R11148	Fibulin A.	9.01e+00
Ο,	96	10.1	601	~	R11149	Fibulin B.	9.01e+00
0,	96	10.1	601	28	W27599	Human fibulin type 1	9.01e+00
	96	10.1	683	7	R11150	Fibulin C.	9.01e+00

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Gaps

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Score 954; DB 30; Length 130; Pred. No. 5.23e-79; 0; Mismatches 0; Indels

Query Match 100.0%; Best Local Similarity 100.0%; Matches 130; Conservative

Human fibulin type 1  Rat hypocretin 35 pep 1.27e+01  Human lecithin-choles 2.10e+01  Natural recombinant b 2.10e+01  Human N-proteinase (7 2.48e+01  Human N-proteinase (7 2.48e+01  Human Secreted protei 2.93e+01  Truncated Platelet de 2.93e+01  Platelet-derived Grow 2.93e+01  Recombinant platelet 2.93e+01  PLOGF Bsis. 2.93e+01  Recombinant platelet 2.93e+01  Recombinant platelet 2.93e+01  HWATO (CVG-2) ICP34.5 3.46e+01  HWATO 4-1BB-L DOLYPEP 3.46e+01  HWATO 4-1BB-L DOLYPEP 3.46e+01  HWATO 4-1BB-L DOLYPEP 3.46e+01  Tryptophan aporepress 3.46e+01  Recombinant platelet 4.08e+01  Human aspartic protea 4.08e+01	ALIGNMENTS  WO0157 W850157 W85015 W850157 W850
W27600 W27600 W2760160 W270160 W270189 W77028 W77028 W770028 W770028 W77009 W77000 W77000 W7700 W7700 W7700 W7700	in; 130 AA.  try)  5; treatment; nn hormone produc hormone produc  ST.  ST.  be Lecea L, E  y De Lecea L, E  y Sutcliffe JG  p; English scauence for c  p; English so rat hypocreti ody temperature receptor can be treeptor can be trides based on its RNA trans pression. The public RNA trans pression. The RNA trans pression and as a pression. The RNA trans pression and as a pression.
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083 703 107 440 440 108 108 108 108 108 108 108 10	(first entry in 35. H35; H35; H35; H35; H35; H35; H35; H35;
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Claim 2; Fig 2; 35pp; English.

The HFGAN72 receptor protein contains two ligands whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulnina, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulinia and cachexia. The HFGAN72 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthm, parkinson's disease, both acute and congestive heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired glucose tolerance, sexual dysfunction and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delinium, dementia, severe mental retardation and dyskinesias such as Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glial cell line-derived neurotrophic factor receptor gamma 1.
Glial cell line-derived neurotrophic factor receptor gamma 1;
GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF,
neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gammal;
Parkinson's disease; schizophrenia; insomnia; tardive dyskenisia;
hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AGILTLGKRRPGPPGLQGRLQRLLQANGNHAAGILTMGRRAGAELEPYPCPGRRCPTATA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 agiltlgkrrsgppglggrlgrllgasgnhaagiltmgrragaepaprpclgrrcsapaa 120
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27-UNN-1997; US-884658.
20-MAY-1997; US-884658.
20-MAY-1997; US-8846792.
GENTZ RJ, HSU T, Ni J, Ruben SM, Young P;
WPI; 99-070150/06.
N-PSDB; V99333.
New isolated glial cell derived neurotrophic factor receptors - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 mnlpstkvswaavtlllllllllppallssgaaaqplpdccrqktcscrlyellhgagnha 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       failure; gut dysfunction; regeneration;
                     WPI; 98-324672/29.
N-PSDB; V28138.
HFGAN72 receptor ligands - and corresponding DNA, agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 782; DB 33; Length 13
Pred. No. 1.76e-62;
10; Mismatches 7; Indels
DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease or Gilles dela Tourett's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= signal_peptide 32..378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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W84185 standard; Protein; 378 AA.
                                                                                              etc.
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Best Local Similarity 85.2%;
Matches 109; Conservative
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                                                                                              antibodies, antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal disorder; kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                          all antibodies, and adjustes, etc.

I all the HFGAN72 receptor protein contains two ligans whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGAN72 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, protension, hypertension, urinary retention, osteoporosis, angina protozis, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired disconse tolerance, sexual dysfunction and psychotic and neurological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure;
sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles dela Tourett's syndrome. Sequence 123 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 vpwaavt11111111ppalls1gvdaqplpdccrqktcscr1yellhqaqnhaaqiltlqk 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 123;
                                                                                                                                                                                                                                                     HFGAN72 receptor ligands - and corresponding DNA, agonists,
antibodies, antagonists, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                       19-MAR-1997; US-820519.
02-UUL-1997; US-887382.
6SMIX ) SMITHKLINE BEECHAM F.C.
(SMIX ) SWITHKLINE BEECHAM P.C.
Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M;
WPI; 98-324672/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 853; DB 33;
Pred. No. 2.73e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
34..66
/note= "Ligand 72A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70..97
/note= "Ligand 72B'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1998.
17-DEC-1997; 310216.
26-SEP-1997; US-993903.
17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-820519.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 5
W61381 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.1%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W61381;
02-OCT-1998 (first entry)
                                                              26-SEP-1997; US-939093
17-DEC-1996; US-033604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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g δy g

g ò Region Region

59

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2; Gaps

DB 33; Length 131;

411

14

Therve cells

Claim 2: Page 85-86; 113pp; English.

This annino acid sequence comprises human Ret ligand (RetL) RetL3,

This annino acid sequence comprises human RetL1, human RetL2 and

Geduced from CDNA clones (see W37457-62) are also claimed. Human

RetL3 is 34.3% identical to human RetL1, human RetL2 and

mouse RetL3 is 34.3% identical to human RetL1, 34.9% identical to human

RetL2 and 76.8% identical to human RetL1, 34.9% identical to human

RetL2 and 76.8% identical to human RetL1, 34.9% identical to human

RetL3 and 76.8% identical to human RetL1, 34.9% identical to human

RetL3 and 76.8% identical to human RetL1, 34.9% identical to human

RetL3 and 76.8% identical to human RetL1, 34.9% identical to human

RetL3 and 76.8% identical to human RetL1, 34.9% identical to human

RetL3 and 76.8% identical to human RetL3, is set ligand is a key

component of the Ret signalling pathway that specifically

interacts with Ret receptor protein, triggering Ret dimerisation

vectors containing retL3 DNA and prokaryotic or eukaryotic host

cells transformed or transfected with these vectors are claimed, as

well as a method for production of RetL3, its soluble variants and

fusion proteins with a toxin, imageable compound or radionuclide.

RetL3, optionally when expressed from vectors in vivo, is used to

promote growth of new tissue and survival of damaged tissue,

particularly kidney or neural tissue. Typical applications are in

renal failure, nephritis, kidney transplants, toxic or hypoxic

injury, neurodegeneration, motor neuron disease, multiple sclerosis,

bacterial, viral or prion infections (e.g. meningitis, myelopathy

associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or

spinal cord injury, developmental disorders such as Down's syndrome

system (Lyme disease, muscular dystrophy and myasthenia gravis).

Fusion proteins are used to deliver toxins etc. to Ret-expressing 3 This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and sequence 400 AA; vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or Gaps New nucleic acid encoding ret receptor ligands and related proteins Human Ret ligand RetL3.

Ret ligand; RetL3. receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldf-Jakob disease; candal nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; 2; Score 113; DB 32; Length 400; Pred. No. 4.63e-01; 9; Mismatches 9; Indels 9 plppvvlm11111ppsplplaa-gdplptesrlmn-sc C, Sanicola-Nadel M; myasthenia gravis; tumour; therapy. II 11 W37463 standard; Protein; 400 AA Query Match 11.8%; Best Local Similarity 47.4%; 21-MAY-1998 (first entry) especially tumours. 18; Conservative 27.NOV-1997. 07.MAY-1997; U07726. 10.APR-1997; US-017427. 08.MAY-1996; US-017427. 07.JUN-1996; US-018930. 16.JUL-1996; US-021859. (BIOJ ) BIOGEN INC. WPI; 98-018431/02. N-PSDB; V00251. Cate RL, Hession Homo sapiens. 27-NOV-1997 W37463; 8888888888 g ŏ

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Sequence
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                                                                                                                                                                                                                                                           Gaps
single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus O-glycosylation sequence. CXCXFC.
Immediately following each repeat is a pentapeptide with the consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the protein have important diagnostic and therapeutic uses. See also R11149 and R11150.
                                                                                                                                                                                                                      Score 96; DB 2; Length 566;
Pred. No. 9.01e+00;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibulin B.
Beta-1 integrin; adhesion; receptor; fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label = N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Glu/Asp-rich region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..29
/label= signal sequence
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/label= repeat unit 3
307..311
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/label= repeat unit 1
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/label= repeat unit 2
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| Jabel = type II motif
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261..265
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/label= repeat unit 4
355..359
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/label= repeat unit 5
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/label= type I motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30..601
/label= fibulin B
                                                                                                                                                                                                                                                                                                                                                                                          R11149 standard; Protein; 601 AA.
                                                                                                                                                                                                                      Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      R11149;
21-MAY-1991 (first entry)
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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

Scalaim 10; Fig 4; 56pp; English.

Claim 10; Fig 4; 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at posn. 566 ( terminal codon in fibulin A)

and 683 residues resp.

All three forms are rich in cysteine (11 %) and 683 residues resp. All three forms are rich in cysteine (11 %)

and analysis wrt no. and spacing of the Cys residues revealed two types of repeat moftif (I and II). The type I motif, CC(X)12c-

C(X)9-10C(X)6CC is repeated twice, separated by an imperfect form of the repeat lacking two Cys residues. The same motif is found in complement components C3a, C4 and C5a; the inverse is found in complement components C3a. The same motif is found in complement components C3a. The same motif is found in complement components C3a. The same motif is found in complement components C3a.

The type II motif, related to repeats found in epidermal growth the city precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats.

C(2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 residue insertion between cysteines 4 and 5 instead of the usual consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus 0-gir/cosylation sequence, CXCXPC.

Immediately following each repeat is a pentapeptide with the consensus of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, faminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses.

Sequence ASP HILM4, XII148 and XII150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Human fibulin type 1 isoform (variant B).

Human fibulin protein; met-OB protein; hypertension; obesity; isoform; type II diabetes; fibrogenesis.

WO9738014-A1.
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5. 9.01e+00;
... 8; Indels
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/label= consensus pentapeptide
                                                                                                                              Tabel = consensus pentapeptide
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Pred. No. 9
                                                                  'label = repeat unit 7
                                                                                                                                                                                                       repeat unit 8
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W27599 standard; Protein; 601 AA.
W27599;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (LJOL-) LA JOLLA CANCER RES. (AMNA-) AMER NAT RED CROSS.
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Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruoslahti EI, Argraves WS;
WPI; 91-087250/12.
N-PSDB; Q11009.
                                                                                                                                                             485..529
/label= re
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03-APR-1997; U06280.
04-APR-1996; US-627636.
(AMGE-) AMGEN INC.
Bennett LG;
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18-AUG-1989; US-395773.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:02:20 1999; MasPar time 11.91 Seconds 595.879 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 40.229; Variance 88.216; scale 0.456 Statistics:

# STIMMARTES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ		SUMMAKIES	2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	
Result No.	Score	Query Match	Query Match Length DB	B ID	Description	Pred. No.
H	954	100.0	130 1	1 055232	PREPRO-OREXIN.	1.31e-153
2	894	93.7	130 1	1 055241	HYPOCRETIN (PREPRO-ORE	3.25e-142
æ	782	82.0	131	4 043612	PREPRO-OREXIN.	4.87e-121
4	756	79.2	131	6 077668	PREPRO-OREXIN PRECURSO	3.82e-116
2	113	11.8		4 060609	GDNF FAMILY RECEPTOR A	5.76e-03
9	106	11.1	679 1	0 023352	HYPOTHETICAL 74.6 KD P	4.77e-02
7	86	10.3	574 1	1 035298	ACYLOXYACYL HYDROLASE.	4.90e-01
80	86	10.3	641 1	1 008463	FRIZZLED PROTEIN HOMOL	4.90e-01
σ	96	10.1	272	5 077465	LARGE RIBOSOMAL PROTEI	8.63e-01
10	96	10.1	626 1	1 070421	FRIZZLED-1.	8.63e-01
11	96	10.1	920	2 087342	BETA-(1-3)-GLUCOSYL TR	8.63e-01
12	92	9.6	106 1	0 041051	PROLINE- AND LEUCINE-R	2.62e+00
13	91	9.5	440 1	1 035849	LECITHIN: CHOLESTEROL A	3.45e+00
14	06	4.6	833	4 099523	SORTILIN PRECURSOR.	4.53e+00
15	88	ъ. 9	144	4 075779	COLIA1 AND PDGFB FUSIO	5.93e+00
16	89	9.3	154	4 015186	COLIA1 AND PDGFB FUSIO	5.93e+00
17	89	9.3	175	4 060895	MRNA ENCODING RAMP2 PR	5.93e+00
18	89	9.3	185	4 Q15354	C-SIS PROTO-ONCOGENE (	5.93e+00
19	88	9.3	331 1	3 091640	LEUCINE ZIPPER WITH BA	5.93e+00
20	88	9.3	1321	4 075129	KIAA0634 PROTEIN (FRAG	5.93e+00
					•	

7.74e+00 7.74e+00 1.01e+01 1.01e+01 1.01e+01 1.01e+01 1.01e+01 1.3
HYPOTHETICAL 23.1 KD P TIGHT JUNCTION PROFEIN V-SIS TRANSFORMING PRO POLYPROTEIN PRECURSOR L-1 METALLO-BETA-LACTA DIPHTHAMIDE BIOSYNTHES DNA BINDING PROTEIN EI SIMILARITY TO MOUSE SM PUTATIVE GPI-ANCHORED LEGGINE-RICH RECEPTOR-NB-2. (STRAIN OREGON) P125 ( POLYRETIDE SYNTHASE MO POLYPROTEIN POLYRETIDE SYNTHASE MO POLYPROTEIN POLYRETIDE SYNTHASE MO NHOA. PORTINE MEMBRANE COFAC PUTATIVE G PROTEIN RE G PROTEIN COUPLED RECE RNA-DEPENDENT RNA POLY ANION EXCHANGER ISOFOR HYPOTHETICAL 33.3 KD P THYROID HORMONE INDUCE
0005319 0095168 00412803 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299 00518299
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226 1174 227 275 275 275 276 276 276 276 276 276 276 276 276 276
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#### ALIGNMENTS

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MEDLINE; 9., HODSON S.A., PATEL, K., MURRHY G., PIFFANELLI P., WEDLER H., MEDLER E., WAMBUTT R., WEITZENEGGER T., POHL T.M., TERRYN N., RADLER E., WAMBUTT R., WEITZENEGGER T., POHL T.M., TERRYN N., RADLER D., SA GIELEN J., VILLARROEL R., VAN MONTAGU M., ECHARNY A., RADLORG S., GY I., KREIS M., LON N., KRANANGH T., HEMPEL S., KOTTER P., STLUYY M., JAMES R., MONTFORT A., PONS A., PINGOMENICH P., DORKA A., RADLORG E., MILLIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B., RADLINE T., DUESTERHOFT A., MOORES T., JONES J.D.G., ENEVA T., MALMER K., BENES V., RECHMAN S., ANSORGE W., COOKE R., BERGER C., RELSENY M., VOEL M., VOELKAERT G., MEWES H.W., KLOSTERMAN S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 74.6 KD PROTETH.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANANE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; RARBIDOPSIS.
                                                                                                                                                                                           120
                                                                                                                                                                                                                  9
                                                                                          Gaps
   Gaps
                                                             MNPPFAKVSWATVTLLLLLLLLPPAVLSPGAAAQPLPDCCRQKTCSCRLYELLHGAGNHA
                                                                                                                                                                                        AGILTLGKRRPGPPGLQGRLQRLLQASGNHAAGILTMGRRAGAEPAPRLCPGRRCLAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L., POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).

EMBL; AF051767; G2961632; --
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Pred. No. 5.76e-03;
   Indels
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EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
   Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 AA; 44538 MW; 6DFB5381 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 47.4%;
Matches 18; Conservative
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         120 TALAPRGG 127
                                                                                                                                                                                                                                                                                                                  SSVAP-GG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998
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01-AUG-1998
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023352
023352;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                   598 KYCRSK-YETIHGONHDNAADVLELAIKREMPAELL-R-ASLRHTNEDQRNFLLNVGRSA 654
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-SPRAGUE-DAWLEY; TISSUE-OSTEOSARCOMA;

MEDLINE; 93094228.

CHAN S.D.H., KARPF D.B., FOWLKES M.E., HOOKS M., BRADLEY M.S.,

VUONG V., BAMBINO T., LIU M.Y.C., ARNAUD C.D., STREWLER G.J.,

NISSENSON R.A.;

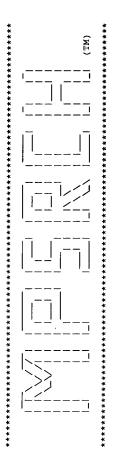
TWO homologs of the Drosophila polarity gene frizzled (fz) are
widely expressed in mammalian tissues.";

J. BIOL. CHEM. 267:25202-25207(1992).

-: FUNCTION: MAY BE INVOLVED IN TRANSDUCTION AND INTERCELLULAR
                          οf
                                                                                                                                                                                          4;
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SCHUELLER C., CHALWATZIS N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 arabidopsis thatiana.";
NATURE 391:485-488(1998).
EMBL; 297337; E326841; -:
                                                                                                                                                     Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 574;
                                                                                                                                                                                        22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6;
MUNFORD R.S., FOSMIRE S., VARLEY A.W., STAAB J.F.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF018172; G2529571; -.
PFAM; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.77e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98; DB 11;
Pred. No. 4.90e-01;
                                                                                                                                                      DB 10;
                                                                                                                   B301B713 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65154 MW; B7D6EE69 CRC32;
                                                                                                                                                                      Pred. No. 4.77e-
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 574 AA.
                                                                                                                                                     Score 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
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SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                   74635 MW;
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05,
08,
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38.1%;
                                                                                                                                                     Query Match 11.1%;
Best Local Similarity 32.3%;
Matches 20; Conservative
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Best Local Similarity 38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q08463;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. ACYLOXYACYL HYDROLASE.
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                                                                                                PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOUSE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 AA;
                                                                                                                   679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                              HYPOTHETICAL
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                                                                                                                   SEQUENCE
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Q08463
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Job time : 42 secs.
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SEQUENCE
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075779
075779;
                                                                                                  SIGNAL.
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acyltransferase.";
BIOCHIM. BIOCHIM. ACTA 1346:207-211(1997).
-!- CATALYIIC ACTIVITY: PHOSCHATIDYLCHOLINE + STEROL = STEROL ESTER +
1-ACYLGLYCEROPHOSPHOCHOLINE.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97166212.
PETERSEN C.M., NIELSEN M.S., NYKJAER A., JACOBSEN L., TOMMERUP N., RASMUSSEN H.H., ROIGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K., "Molecular identification of a novel candidate sorting receptor
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARKS J.S.;
rat lecithin:cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 440;
                                                                                                                                                                                                                                     Length 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91; DB 11; Length 440
Pred. No. 3.45e+00;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                     4; Indels
                                                                                           TISSUE-PERICARP;
RODRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELTRAN J.;
SUBRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELTRAN J.;
SUBRITTED (NOV-1955) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z67873; E208986; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
LECTIVIIN: CHOLESTEROL ACYLTRANSFERASE (EC 2.3.1.43)
(PHOSPHATIDYLCHOLINE--STEROL O-ACYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY, AND WISTAR; TISSUE-LIVER, MEDLINE; 97363611.
WANG J., GEBRE A.K., ANDERSON R.A., PARKS J.S.;
"Cloning and in vitro expression of rat lecithin
                                                                                                                                                                                                                                  Score 92; DB 10;
Pred. No. 2.62e+00;
4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LECITHIN--CHOLESTEROL ACYLTRANSFERASE) (LCAT) (PHOSPHOLIPID--CHOLESTEROL ACYLTRANSFERASE).
                                                                                                                                                                                    11828 MW; A45AD924 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49882 MW; 6CC16087 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      833 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGLPGS--PWQWVLLLLGLLLPPA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U62803; G2306762; -.
PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNLPSTKVPWAAVTLLLLLLLPPA 24
                                                                                                                                                                                                                                                                                                                                                        72 ILLLLLLPPPLLLLLMRPLPL 92
                                                                                                                                                                                                                                  Query Match 9.6%;
Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03,
03,
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Best Local Similarity 62.5%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
                                                                                                                                                                                       106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SORTILIN PRECURSOR
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                    SEQUENCE
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Q99523
Q99523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 13
035849
035849;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         Gaps
purified from human brain by receptor-associated protein affinity
                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 144;
                                                                                                                                                                Length 833;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'BRIEN K.P.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y15921; E1309800;
                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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9
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Pred. No. 5.93e+00;
11; Mismatches 6
                                                                                                                                                                Score 90; DB 4; L. Pred. No. 4.53e+00;
                                                                                                       SORTILIN.
; D2E351B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDA
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UP
COLIAL AND PDGFB FUSION TRANSCRIPT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 144
144 AA; 15626 MW; AF87E707 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 LQRLLHGDPGEEDGAELDLNMTRSHSGGELESLA-RGRR
                                                                                                                                                                                                     5; Mismatches
                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                              10 WA-AVTLLLL-LLPPALLSLG-VDAQPLP 36
                                                                                                                                                                                                                                         14 WPHGLGLLLLLQLLPPSTLSQDRLDAPPPP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Fri Aug 20 21:03:02 1999
                chromatography.";
J. BIOL. CHEM. 272:3599-3605(1997).
EMBL; X98248; E246784; -.
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                        33 PC
833 SC
92408 MW;
                                                                                                                                                              Query Match 9.4%;
Best Local Similarity 53.3%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.3%;
Local Similarity 43.6%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                         34 8
833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:01:51 1999; MasPar time 6.13 Seconds 599.747 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130

Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

swiss-prot37 1:swissprot Database:

Mean 41.950; Variance 76.092; scale 0.551 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	1.07e-02	2.12e-02	1.12e-01	1.12e-01	1.12e-01	1.12e-01	1.12e-01	2.97e-01	2.97e-01	5.61e-01	5.61e-01	5.61e-01	1.05e+00	1.05e+00	1.05e+00	1.43e+00	1.43e+00	1.43e+00	1.94e+00	2.64e+00	2.64e+00	2.64e+00	2.64e+00
Description	GLYCOPROTE	SECRETIN PRECURSOR (FR	PHOSPHATIDYLCHOLINE-ST	FIBULIN-1, ISOFORM A P	FIBULIN-1, ISOFORM B P	FIBULIN-1, ISOFORM C P	FIBULIN-1, ISOFORM D P	FIBRIL-FORMING COLLAGE	ATRIAL NATRIURETIC PEP	COMPLEMENT C1Q SUBCOMP	PHOSPHATIDYLCHOLINE-ST	PHOSPHATIDYLCHOLINE-ST	PLATELET - DERIVED GROWT	SALIVARY PROLINE-RICH	PROSTAGLANDIN G/H SYNT	INFECTED CELL PROTEIN	4-1BB LIGAND (4-1BBL).	SEC14 CYTOSOLIC FACTOR	PDGF-RELATED TRANSFORM	INFECTED CELL PROTEIN	RIBOSOMAL LARGE SUBUNI	FERRIC ENTEROBACTIN TR	PHOSPHATIDYLCHOLINE-ST
ΙD	GPV_RAT	SECR_PIG	LCAT_MOUSE	FBLA_HUMAN	FBLB_HUMAN	FBLC_HUMAN	FBLD_HUMAN	CAFF_RIFPA	ANPA_HUMAN	C1QB_HUMAN	LCAT_RAT	LCAT_HUMAN	PDGB_HUMAN	PRP1_HUMAN	PGH1_RAT	ICP3_HSV1D	41BL_HUMAN	SC14_YARLI	TSIS_SMSAV	ICP3_HSV1N	RLUC_HAEIN	FEPD_ECOLI	LCAT_PAPAN
DB	П	-	Н	П	Н	Н	Н	۲	Н	Н	Ч	Н	Н	~	Н	Ч	Н	Н	Н	Н	Н	Н	Н
% Query Match Length	567	131	438	266	601	683	703	1027	1061	251	440	440	241	331	602	252	254	497	226	245	322	334	440
% Query Match	10.8						Н			9.5	9.5	9.5	9.3	9.3	9.3	φ.	9.	o,	9.1	σ.	9.	0.6	
Score	103	101	96	96	96	96	96	93	93	91	16	91	68	68	68	88	88	88	87	86	86	98	86
Result No.	н.	7	m	4	S	9	7	ω	σ	10	11	12	13		15		17		19			22	23

2.64e+00	2.64e+00	3.56e+00	3.56e+00	3.56e+00	3.56e+00	4.80e+00	6.46e+00	6.46e+00	6.46e + 00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00							
RETINAL GUANYLYL CYCLA	COMPLEMENT C3 PRECURSO	PLACENTAL LACTOGEN I P	PLATELET - DERIVED GROWT	HYPOTHETICAL 28 KD PRO	LIPASE 1 PRECURSOR (EC	LYSIS PROTEIN (E PROTE	LYSIS PROTEIN (E PROTE	EPHRIN-A3 PRECURSOR (E	LIPASE 3 PRECURSOR (EC	RIBOSOMAL LARGE SUBUNI	GIPASE ACTIVATING PROT	LUTROPIN-CHORIOGONADOT	PROTEIN-TYROSINE PHOSP	OXALATE OXIDASE PRECUR	SL CYTOKINE PRECURSOR	PUTRESCINE TRANSPORT S	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL 59.6 KD P	PROTEIN-TYROSINE PHOSP	RETINAL GUANYLYL CYCLA	ANGIOTENSIN-CONVERTING
CYGD_HUMAN	CO3_RAT	PLC1_BOVIN	PDGB_MOUSE	YPE1_RHORU	LIP1_PSYIM	VGE_BPPHX	VGE_BPS13	EFA3_HUMAN	LIP3_MORSP	RLUC_ECOLI	RN_DROME	LSHR_PIG	PTPX_MOUSE	OXO2_HORVU	FL3L_HUMAN	POTI_ECOLI	LCAT_RABIT	YABK_ECOLI	PTPX_RAT	CYGD_CANFA	ACE_RABIT
Н	Н	Н	-	Н	Н	Н	Н	Н	Н	ч	Н	Н	н	1		<del>, ,</del>	Н	Н	Н	Н	Н
1103	1663	236	241	255	317	90	90	238	315	319	384	969	1001	224	235	281	440	536	1004	1109	1310
9.0	0.6	8.0	6.8	ø.	8.9	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7
. 98	98	82	82	82	82	84	84	84	84	84	84	84	84	83	83	83	83	83	83	83	83
24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

### ALIGNMENTS

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TLLLLLLLPPALLSLGVDAQPLP 36

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                                                                                                                                                                                                                                                                                                                                                                                    MERONI G., MALGARETTI N., MAGNAGHI P., TARAMELLI R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
                                                                                                                                                                                                                                                                                      "Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin: cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver."; J. BIOL. CHEM. 264:21573-21581(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A341158; XXMSN.
MGD; MGI:96755; LCAT.
PROSITE: PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL ESTER 1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CP BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                           01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                        MEDLINE; 90094326.
WARDEN C.H., LANGNER C.A., GORDON J.I., TAYLOR B.A., MCLEAN J.W.
                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 96; DB 1; Length 438;
Pred. No. 1.12e-01;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9E6B904A CRC32;
                438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                              CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%;
ilarity 62.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J05154; G293697; -.
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438
205
98
380
44
108
296
397
                                          01-AUG-1990 (REL. 15,
01-AUG-1990 (REL. 15,
01-NOV-1997 (REL. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X54095; G52874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT AS ACCEPTOR)
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108
296
397
408
438 AA;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION THIS ENZYME.
                                                                                                                             ACYLTRANSFERASE)
LT 3
LCAT_MOUSE
P16301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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(POTENTIAL).
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ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;
"Fibulin, a novel protein that interacts with the fibronectin receptor bette subunit cytoplasmic domain.";
-1. 58:623-629(1989).
-1. SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-1. ALTERNATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (SHOWN HERE), B (A P23143), C (AC P23144) AND D (AC P37888); DIFFERING ONLY IN THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
-1. SIMILARITY: CONTAINS 8 COMPLETE AND ONE INCOMPLETE EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.
                                                                                                                                                                                  EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
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            566 AA
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EGF-LIKE 2, C
EGF-LIKE 3, C
EGF-LIKE 5, C
EGF-LIKE 5, C
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EGF-LIKE 6, C
EGF-LIKE 7, C
EGF-LIKE 8, C
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PROSITE: PS00102; BGF_1; FALSE_NBG.
PROSITE: PS01177; ANAPHYLATOXIN_1; 3.
PROSITE: PS01178; ANAPHYLATOXIN_2; 3.
PROSITE: PS01186; BGF_2; 3.
PROSITE: PS01187; BGF_CA; 8.
PRAM: PF00008; EGF; 5.
HSSP; P35555; 1EMO.
                                                                        FIBULIN-1, ISOFORM A PRECURSOR
                                    20, CREATED)
20, LAST SEQ
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            STANDARD;
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A36346; A36346.
                                   01-NOV-1991 (REL. 01-NOV-1991 (REL.
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BY SIMIL
                                                                           FIBULIN-1, ISOFORM C.
3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
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PROSITE; PS01187; EGF_CA; 8.
PFAM; PF00008; EGF; 5.
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MEDLINE; 91100426.
ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
A.Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.";
J. CELL BIOL. 111:3155-3164(1990).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM C PRECURSOR.
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PIR; C36346; C36346.

MM; 135820; PSO0010; ASX_HYDROXXL; 4.

PROSITE; PSO0022; EGF_1; FALSE_NEG.

PROSITE; PSO1177; ANAPHYLATOXIN_1; 3.

PROSITE; PSO1177; ANAPHYLATOXIN_1; 3.

PROSITE; PSO1186; EGF_2; 3.
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                           RESULT
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                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LOS. TRANS. R. SOC. LOND., B, BIOL. SCI. 306:345-354(1984).

FUNCTION: C10 ASSOCIATES WITH THE PROBNZYMES C1R AND C1S TO YIELD

EUNCTION: C10 ASSOCIATES WITH THE PROBNZYMES C1R AND C1S TO YIELD

C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE

COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT

C1R(2)C1S(2) PROBNZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1

TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE

FC REGIONS OF IGG ANTIBODY PRESENT IN IMMONE COMPLEXES.

SUBJUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q,

R AND S IN THE MOLAR RATION OF 1:2:2.

SUBJUNIT: C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF
                                                                                                                                                                                                          WHICH ARE DISULFIDE-LINKED DIMERS OF THE A & B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN.
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PFAM; PF00386; C1q; 1.
COMPLEMENT PATHWAY; PLASMA; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN;
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Pred. No. 5.61e-01;
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N REF. 2).
N REF. 2 AND 3).
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PIR; B23422; B23422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.

CATALVITC ACTIVITY: PROSPHATIDYLCHOLINE + STEROL = STEROL ESTER + I-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                        01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             MERONI G., MALGARETTI N., MAGNAGHI P., TARAMELLI R.; "NUCLEOTIGE sequence of the CDNA for lecithin-cholesterol acyl transferase (LCAT) from the rat."; NUCLEIC ACIDS RES. 18:5308-5308(1990).
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                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHÓKDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
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(REL. 04, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDAT
                                                                                  LAST SEQUENCE UPDATE)
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MEDLINE; 97141927.

SIMON M.-P., PEDEUTOUR F., SIRVENT N., GROSGEORGE J., MINOLETTI F., COINDRE J.-M., TERRIER-LACOMBE M.-J., MANDALL N., CRAVER R.D., BLIN N., SOZIG G., TURC-CAREL C., O'BRIEN K.P., KEDRA D., "PRANSSON I., GUILBAUD C., DUMANSKI J.P.; "Deregulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans
                                                                     WONG-STAAL F.;
"Transforming potential of human c-sis nucleotide sequences encoding platelet-derived growth factor.";
SCIENCE 225:636-639(1984).
                                                                                                                                                                                                                     RAO C.D., IGARASHI H., CHIU I.-M., ROBBINS K.C., AARONSON S.A.;
Structure and sequence of the human c-sis/platelet-derived growth
factor 2 (SIS/PDGF2) transcriptional unit.":
PROC. NATL. ACAD. SCI. U.S.A. 83:2392-2396(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLLINS T., GINSBURG D., BOSS J.M., ORKIN S.H., POBER J.S.;
Cultured human endothelial cells express platelet-derived growth
factor B chain: cDNA cloning and structural analysis.";
NATURE 316:748-750(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEICH HUMAN SEBALD W., SCHAIRER H.U., HOPPE J.;
"The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which codes for the sequence of the PDGF-B chain.";
FEBS LETT. 198:344-348(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAO C.D., IGARASHI H., PECH M.W., ROBBINS K.C., AARONSON S.A.; "Oncogenit potential of the human platelet-derived growth factor transcriptional unit...; COLD SPRING HARB. SYMP. QUANT. BIOL. 51:959-966(1986).
                                                                                                                                                                                                                                                                                                                                                                             -M., REDDY E.P., GIVOL D., ROBBINS K.C., TRONICK S.R.,
                                               JOSEPHS S.F., RAINER L., CLARKE M.F., WESTIN E.H., REITZ M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence analysis identifies the human c-sis
proto-oncogene as a structural gene for platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 84236121.
JOHNSSON A., HELDIN C.H., WASTESON A., WESTERMARK B.,
HUANG J.S., SEEBURG P.H., GRAY A., ULLRICH A., SCRACE
STROOBANT P., WATERFIELD M.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BURGESS J., ODELL C.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAINER L. JOSEPHS S.F., JARRETT R., REITZ M.S., "Nucleotide sequence of transforming human c-sis homology to platelet-derived growth factor."; NUCLEIC ACIDS RES. 13:5007-5018(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and giant-cell fibroblastoma.";
NAT. GENET. 15:95-98(1997).
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                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 22-241 FROM N.A. MEDLINE; 84205633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL 37:123-129(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 85296313
                                                                                                                                                                                                   MEDLINE; 86205961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 85269623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86164981
                        MEDLINE; 84250225
                                                                                                                                                                                                                                                                                                                                                                                                 AARONSON S.A.;
                                                                 WONG-STAAL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                        HUM. MUTAT. 8:79-82(1996).

-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTEROL TRANSPORTED IN PLOPROFIEINS.

-!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL ESTER + 1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERED). A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
"Complete deficiency of plasma lecithin-cholesterol acyltransferase (LCAI) activity due to a novel homozygous mutation (Gly-30-Ser) in
                                                                                                                                                                                                                  ACT AS ACCEPTOR). ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LECITHIN-CHOLESTEROL ACYLTRANSFERASE. CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                      DISEASE: DEFECTS IN LCAT ARE THE CAUSE OF NORUM AND FISH EYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
PDGF-2) (BACAPLERMIN).
PDGFB OR C-SIS.
HOMO SAPIENS (GUMAN).
PURARYOTA: METAZOA: CORDATA; VERTEBRATA: MANMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                  LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X06537; -; NOT_ANNOTATED_CDS.
BMBL; MSC568; GB7025; -
EMBL; X04981; G34287; -
EMBL; M17959; G386858; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE MUTATION.
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P01127; P78431;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQI
15-DEC-1998 (REL. 37, LAST ANNO
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81.3%;
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PIR; A29661; A29661.
PIR; A25575; A25575.
PIR; JQ0036; JQ0036.
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Matches 13; Conser
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205
74
337
                                                                                                                                                                                                                                                                 THIS ENZYME
                                        the LCAT gene.
HUM. MUTAT. 8:
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MIM; 245900;
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DISULFID
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Query Match

pp δy RESULT
1D PD
AC P10
DT 21
DT 21
DT 21
DT 21
DT 60
DE PL
CO PN
RN P1
RN P1
FN P

DISULFID CARBOHYD CARBOHYD CARBOHYD

SIGNAL CHAIN

WONG-STAAL F.; CDNA clones with

growth

DEUEL T.F., G.,

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BIOCHEM. BIOPHYS. 307:361-368(1993).
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ACT_SITE
BINDING
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                           SAITOH E., ISEMURA S., SANADA K.;
"Further fractionation of basic proline-rich peptides from human parotid saliva and complete amino acid sequence of basic proline-rich J. BIOCHEM. 94:1991-1997/1002>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGH1_RAT STANDARD; PRT; 602 AA.

063921; 062731; 063684;

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE 1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN-HASE 1) (PGH SYNTHASE 1) (PGH SYNTHASE 1) (PHS 1).

PTGS1 OR COX1 OR COX-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 94099619.
FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,
WILSON C.B., HWANG D.;
"Cloning two isoforms of rat cyclooxygenase: differential regulation of their expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLILLSVALLALS-SAQNLNEDVSQEE-S-P--SLIAGNP-QGPSPQG-GNKPQGPPPP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                   KAUFEMAN D., HOFMANN T., BENNICK A., KELLER P.;
"Basic proline-rich proteins from human parotid saliva: complete covalent structures of proteins IB-1 and IB-6.";
BIOCHEMISTRY 25:2387-2392(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: | : : : : : : |: |: OGRLQRLLQANGNHAAGILTMGRRAGAELEPYPCPGRRCPTATATALAPRGGSR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 PGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGDKSRSPRSPPGKPQGPPPQGGNQ 107
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89; DB 1; Length 331;
Pred. No. 1.05e+00;
26; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT; PAROTID GLAND; MULTIGENE FAMILY; SALIVA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE IB-6.
PEPTIDE P-H.
MISSING (IN CLONE CP-4).
MISSING (IN CLONE CP-5).
A -> S (IN REF. 2 AND 3).
W; D18DE589 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K03204; G190486; -.
EMBL; K03205; G190504; -.
EMBL; K03206; G190506; -.
PIR; A03291; PIHUB6.
PIR; C25372; C25372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331
238
258
276
                   SEQUENCE OF 214-331.
                                                                                                                                                         SEQUENCE OF 276-331.
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276
106
106
276
331 AA;
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                                     86243355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
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CONFLICT
SEQUENCE
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-!- THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-!- THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
SEQUENCE FROM N.A.
STRAINFISHER 344; TISSUE=TRACHEA;
MEDLINE, 95168876.
KITZLER J., HILL E., HARDMAN R., REDDY N., PHILPOT R., ELING T.E.;
"Analysis and quantitation of splicing variants of the TPA-inducible PGHS-I mRNA in rat tracheal epithelial cells.";
ARCH. BIOCHEM. BIOPHYS. 316.856-863(1995).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                   -! - CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2, O(2) = PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
ASPIRIN-ACETYLATED SERINE.
BY SIMILARITY.
POTEWITAL.
POTEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : PEROXIDASE; GLYCOPROTEIN; ACETYLATION; HEME; IRON; SIGNAL; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                      H2 + A + H(2)O.
-!- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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PROSTAGLANDIN G/H SYNTHASE 1.
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 602;
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REF. 1).
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EMBL; S67721; G466556; -
EMBL; U18060; G603052; -.
PROSITE; PS00022; EGF_1; FALSE_NEG-
PROSITE; PS01186; EGF_2; FALSE_NEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
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PROSTAGLANDIN BIOSYNTHESIS; H
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Best Local Similarity 40.0%;
Matches 16; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:01:12 1999; MasPar time 8.58 Seconds 607.078 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALALAPRGGSRV 130 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

122810 segs, 40068593 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 40.689; Variance 84.298; scale 0.483 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	1.96e-02	9.12e-02	1.23e-01	2.25e-01	4.07e-01	4.07e-01	4.07e-01	9.78e-01	9.78e-01	1.74e+00	1.74e+00	1.74e+00	1.74e+00	3.06e+00	3.06e+00	3.06e+00	3.06e+00	3.06e+00	3.06e+00	4.05e+00	4.05e+00	4.05e+00	4.05e+00
Description	hypothetical protein	secretin precursor -	catalase (EC 1.11.1.6	probable intercellula	phosphatidylcholine	fibulin 1 precursor,	fibulin 1 precursor,	collagen alpha chain	natriuretic peptide r	complement subcompone	phosphatidylcholine	phosphatidylcholine	cyclooxygenase 1 - ra	hypothetical protein	platelet-derived grow	platelet-derived grow	salivary proline-rich	prostaglandin G/H syn	cal prote	probable cutinase pre	ligand (	4-1BB ligand - human	stromelysin 3 (EC 3.4
ID	C71413	SEPG	JA0091	A45054	XXMSN	B36346	C36346	S28774	OYHUAR	CIHUQB	XXRIN	XXHUN	S39782	S58383	A55030	PFHUG2	PIHUB6	S69198	T00382	A70565	S43293	138427	JC6197
DB	7	Н	7	~	Н	7	N	7	Н	П	<b>~</b>	Н	7	~	N	Н	Н	7	7	N	7	~	7
Length	629	131	495	641	438	601	683	1027	1061	253	440	440	602	185	230	241	392	602	1321	226	245	254	491
% Query Match	11.1	10.6	10.5	10.3	10.1	10.1	10.1	7.6	7.6			٠	9.5	9.3	6.9		٠	9.3	٠	9.5		9.5	
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7.03e+00 9.24ee+00 9.24ee+00 9.24ee+00 9.24ee+00 9.24ee+00 9.24ee+00 1.21ee+00 1.21ee+01 1.21ee+	complement (3 precurs 7 03e placental lactogen pr 9.24e platelet-derived grow 9.24e triacylglycerol lipas 9.24e triacylglycerol lipas 9.24e triacylglycerol lipas 9.24e probable nhoA protein 9.24e ndothelin receptor t 9.24e hypothetical protein 9.24e gene E protein - phag 1.21e lutropin-choriogonado 1.21e lutropin-choriogonado 1.21e lutropin-choriogonado 1.21e tre  Arabidopsis thaliana Arabidopsis thaliana #common name mouse-ear	S T T T T T T T T T T T T T T T T T T T	4 2000000000000000000000000000000000000	1663 236 241 241 241 317 317 317 911 911 329 329 339 331 311 311 311	9.0 1 8.9 8 8.9 8 8.9 8 8.9 8 8.8 8 8.8 8 8.8 8 71413 hypothe	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	33 34 35 36 37 37 39 40 44 44 45 ENTRY TITLE ORGANISM
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7.03e+00 7.03e+00	phosphatidylcholine guanylate cyclase (EC	JC1502 JH0717	00-	1102		989	32 T
	hypothétical protein ferric enterobactin t	G64151 S16296	0 0	322 334		86 86	30
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00000	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	. 372673	r	407		a	**

C71413 #type complete hypothetical protein - Arabidopsis thaliana #formal_name Arabidopsis thaliana #common_name mouse-ear cress columbia 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998	C71413 A71400 Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.; Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel, K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Glelen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.; Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.; Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Punk, B.; Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka, A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.; Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.; Moores, T.; Jones, J. D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny, M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.; Schneller	Na An erence C7 s	<pre>##residues</pre>	Query Match 11.1%; Score 106; DB 2; Length 679; Best Local Similarity 32.3%; Pred. No. 1.96e-02; Matches 20; Conservative 16; Mismatches 22; Indels 4; Gaps 4;
RESULT 1 ENTRY TITLE ORGANISM #variety DATE	ACCESSIONS REFERENCE #authors	#journal #title #cross-refe #accession ##status ##molecu	##residues ##cross-re GENETICS #map_position SUMMARY	Query Match Best Local Matches

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#Journal J. Biol. Chem. (1989) 264:21573-21581

#title Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin:cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver.
                                                                                                                                                                                        #accession A34150
#accession A34150
##molecule_type mRNA
##residues 1-438 ##label WAR
##residues GB:05154; NID:9198759; PID:9293697
##cross-references GB:05154; NID:9198759; PID:9293697
##cross-references GB:05154; NID:9198759; PID:9293697
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Promoter and 5' flanking sequences of the mouse LCAT gene. $21370
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#status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K. J. Cell Biol. (1990) 111:3155-3164
Fibulin is an extracellular matrix and plasma glycopro with repeated domain structure.
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#length 438 #molecular-weight 49765 #checksum 1794
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Pred. No. 4.07e-01;
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##cross-references GB:X53742; NID:g31416; PID:g31417
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#map_position 22413.3.22413.3
CLASTECATION #superfamily EGF homology
KEYWORDS alternative splitsing
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                                A34158; S21370
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Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E. Cell (1989) 58:623-629
Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
J. Cell Biol. (1990) 111:3155-3164
Fibulin is an extracellular matrix and plasma glycoprotein
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#product fibulin 1 splice form C #status predicted
#label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
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19.Apr-1991 #sequence_revision 19-Apr-1991 #text_change
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22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change
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#length 683 #molecular-weight 74475 #checksum 7443
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fibulin 1 precursor, splice form C - human
fibulin C
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##cross-references GB:X53743; NID:g31418; PID:g31419
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##residues 1-566 ##label AR2
##cross-references GB:X53741; NID:g31414; PID:g31415
#domain EGF homology #label EGF
#length 601 #molecular-weight 65485
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#map_position 22q13.3-22q13.3
KEYWORDS alternative splicing; glycoprotein
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#cross-references MUID:91100426
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Pred. No. 4.07e-
3; Mismatches
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ilarity 57.1%; F
Conservative
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                                                                                      Best_Local Similarity 57.1%;
Matches 16; Conservative
                                                                 10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
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GENETICS

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Reid, K.B.M.; Thompson, E.O.P.
Biochem. J. (1978) 173:863-868
Amino acid sequence of the N-terminal 108 amino acid residues of the B chain of subcomponent C1q of the first component of human complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The first component of complement is a calcium-dependent complex of the three subcomponents Clq, Clr, and Cls. Subcomponent Clq binds to immunoglobulin complexes, with resulting serial activation of Clr (enzyme), Cls (proenzyme), and the other eight components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #Ecross-references GDB:119043; OMIM:120570
#map_position 1p36.3-1p34.1
CLASSIFICATION #superfamily complement subcomponent Ciq chain A; complement Clq carboxyl-terminal homology
KEYWORDS complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline; plasma; pyroglutamic acid; triple helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *product complement subcomponent Clq chain B *status experimental *label MAT\
*domain collagenous, triple helix *label COL\
#domain complement Clq carboxyl-terminal homology *label
                                                                                                                                                                                                                                                                                                  Reid, K.B.M.; Gagnon, J.; Frampton, J.
Bloochen. J. (1982) 203:559-569
Completion of the amino acid sequences of the A and B chains
of subcomponent Clq of the first component of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXTN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #modified_site pyrrolidone carboxylic acid (Gln) (ir
mature form) #status experimental\
#disulfide_bonds interchain (to chain A-26) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              experimental\
#binding_site carbohydrate (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 253 #molecular-weight 26722 #checksum 7399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Cig subcomponent is composed of nine subunits, six of disulfide-linked dimers of the A (see PIR:CHHUQA) and B and three of which are disulfide-linked dimers of the C PIR:CHHUQC) chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #modified_site 4-hydroxyproline (Pro) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #modified_site 5-hydroxylysine (Lys) #status
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  'E',29-84,'D',86-99,'P',101-135 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91; DB 1; Le
Pred. No. 1.74e+00;
                                                                                                                                                                                                                      ##molecule_type protein
##residues 28-99,'P',101-195 ##label RE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176-Glx may also be present
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##residues 136-253 ##label RE4
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#accession B90315
                                                                                                                                                                             #cross-references MUID:79041552
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Local Similarity 53.3%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           complement
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7 KVPWAAVTLLLLLL 21
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83,86,101,104,107
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     ##residues
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#journal
#title
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#authors
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#title Molecular cloning and characterization of the complementary
DNA and gene coding for the B-chain of subcomponent Clq of
#cross-references MUID:86076906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regions present in subcomponent Clq of the first component of human complement. #cross-references MUID:80020137
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                                           #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'HS',1-32 ##label REI
the authors translated the codon AGT for the second
position as Arg; they were uncertain about the
location of the initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the authors translated the codon ACA for residue 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. J. (1979) 179:367-371
Complete amino acid sequences of the three collagen-like
                                                                                                                                                                                                                                                                                                                      #product natriurefic peptide receptor A #status
predicted *label MAT\
#domain extracellular #status predicted #label EXT\
#domain natriuretic peptide-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain transmembrane #status predicted #label TMMN, #domain intracellular #status predicted #label INTN, #domain protein kinase homology #label KINN, #domain guanylate cyclase catalytic domain homology
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#length 1061 #molecular-weight 118918 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%; Score 93; DB 1; L
larity 48.6%; Pred. No. 9.78e-01;
Conservative 6; Mismatches 10
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##residues 28-253 ##label RE1
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##experimental_source retina
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##molecule_type protein
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##molecule_type DNA
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les 17; Conser
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386,427
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RESULT

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Matches

SUMMARY

ACCESSIONS REFERENCE #authors

ORGANISM

495-1061 526-808 828-1055

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#authors #journal

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SUMMARY
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    ACCESSIONS
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                                                                                                          #title
                       REFERENCE
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                                                                                                                                           catalyzes the transfer of sn-2 fatty acyl groups from phosphatidylcholine (lecithin) to sterol to form sterol fatty esters and lacylglycerphosphocholine palmitcyl, oleoyl, and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as
                                                                                                                                                                                                                                                                              #superfamily phosphatidylcholine--sterol acyltransferase
acyltransferase; cholesterol; glycoprotein; lipid metabolism;
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Apolipoprotein A-I (see PIR:LPHUA1) is a potent activator of this
                                                                                                                                                                                                                                                                                                                                                            #domain signal sequence #status predicted #label SIG(
#product phosphatidylcholine--sterol acyltransferase
#status experimental #label MAT(
#status experimental #label MAT(
#binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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hypochetical protein 2 - human
hypochetical protein 2 - human
fformal_name Homo sapiens #common_name man
12_Feb-1998 #sequence_revision 20-Feb-1998 #text_change
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#molecule_type mRNA
##molecule_type mRNA
##residues 1-602 ##label FEN
##cross-references GB.567721; NID:9460555; PID:9460556
##cross-references GB.567721; NID:9460555; PID:9460556
#length 602 #molecular-weight 69168 #checksum 6900
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Pred. No. 1.74e+00;
0; Mismatches 3; Indels
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                                                                          ##cross-references GDB:119359; OMIM:245900
#map_position 16q22.1-16q22.1
FUNCTION
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Best Local Similarity 40.0%;
Matches 16; Conservative
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Local Similarity 81.3%;
es 13; Conservative
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                                                               GDB: LCAT
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Best Local
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REFERENCE
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ORGANISM
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                                                                 #gene
                                                                                                                                                                                                                                                                                                                                           FEATURE
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ENTRY
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##cross-references GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562 FICATION #superfamily platelet-derived growth factor #length 230 #checksum 3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnsson, A.; Heldin, C.H.; Wasteson, A.; Westermark, B.; Deuel, T.F.; Huang, J.S.; Seeburg, P.H.; Gray, A.; Ullrich, A.; Scrace, G.; Stroobant, P.; Waterfield, M.D. EMBO J. (1984) 3:921-928
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Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. (1995) 23:2815-2822
A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A55030 #type fragment
platelet-derived growth factor chain B precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Homo sapiens #common_name man
18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change
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                                                                                                                                                                                      ##status preliminary
##molecule_type mRNA
##molecule_type mRNA
##residues 1-185 ##label DIR
##cross-references FMBL:X83705; NID:9951023; PID:9951025
CLASSIFICATION #superfamily platelet-derived growth factor
#length 185 #molecular-weight 20774 #checksum 2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title The c-six gene encodes a precursor of the B chain of platelet derived growth factor.
#cross-references MUID:84236121
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Pred. No. 3.06e+00;
...matches 6; Indels
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LORILIQAN-GNH-AAGI-LIMGR-RAGAELEPYPCPGRR 113
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Pred. No. 3.06e+00;
11; Mismatches 6
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Best Local Similarity 43.6%;
Matches 17; Conservative
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Best Local Similarity 43.6%;
Matches 17; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:04:31 1999; MasPar time 2.87 Seconds 459.570 Million cell updates/sec Run on:

Tabular output not generated.

1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALAPRGGSRV 130 >US-08-938-548B-6 (1-130) from US08938548B.pep 954 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

106580 seqs, 10152877 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Mean 28.030; Variance 126.736; scale 0.221 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Pred. No.	7.65e+00	1.26e+01	1.26e+01	1.26e+01	1.49e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	2.44e+01	2.44e+01	2.44e+01	2.44e+01	2.88e+01	2.88e+01	2.88e+01	2.88e+01	3.39e+01	3.39e+01	3.39e+01	3.98e+01	5.50e+01	5.50e+01
	ac	. 5175255.	9, Applicatio	5194596.	4, Applicatio	4, Applicatio	. 5498600.		. 5175255.	1, Applicatio	13, Applicati	2, Applicatio	2, Applicatio	3, Applicatio	5, Applicatio	2, Applicatio	2, Applicatio	3, Applicatio		6, Applicatio	6, Applicatio	. 5219739.	4, Applicatio	4, Applicatio
	Description	Patent No.	Sequence	Patent No	Sequence 4		Patent No	Patent No.	Patent No	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	_	Sequence (		Patent No	Sequence 4	
	ID	5175255-4	PCT-US96-0	5194596-15	US-08-387-	US-08-236-	5498600-2	,	5175255-8	US-08-445-	US-08-469-	PCT-US94-1	us-08-465-		US-08-299-	US-08-453-	0	US-08-026-	US-08-243-	PCT-US94-0	US-08-993-	5219739-15	us-07-794-	US-08-001-
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æ,	Query Match	9.6	9.3	9.3	9.3	9.5	9.1	9.1	9.1	9.1	•	8.9	8.9	•	8.8	•	8.8	•	8.7	8.7	8.7	8.6	8.4	8.4
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US-08-408- US-08-555- US-07-668- PCT-US91-0 US-08-429- US-08-693- US-08-693- US-08-693- US-08-08- US-08-08- US-08-08- US-08-08- US-08-097- US-08-254- US-08-257- US-0	LIGN PRT; ODS SSOI	Pred. NG 10; Miss 10; Miss RSHSGGELE R-:1 1   R-RAGAELE RD; F TUS96090C /TUS96090C /TUS96090C
1001001113011000031300	RD; Son, Arl ON: METH CES: 9 ION DATA MBER: U 3-MAR-19 6810 MW;	6.2%; P. tive 11 LDLNMTRS: 1[TMGR-] 1[TMGR-] 1[TMGR-] 1[TMGR-] 1[TMGR-] 0n PC/TU 1 AL. 1 AL. 1 AL. 1 AL. 2 BY. ES: 10 DRESS: CHI, STE
501 684 1337 589 589 589 6442 4442 11184 11184 11187 1187 1187 1187 1187 1187 1187 1187 1187 1187 1187 1187 1187 1187 11	STANDARD; 5255. Thomason NVEWION: FACION SEQUENCES SEQUENCES ATE: 23-M ATE: 23-M AA; 2681	lailty 46.2%; Conservative DEGERGARELDLINM I -
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TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                          APPLICANT: Thomason, Arlen R.;Nicholson, Margery
TILLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.1%; Score 87; DB 4; Length 241;
Best Local Similarity 43.6%; Pred. No. 1.76e+01;
Matches 17; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length 241;
 Query Match 9.1%; Score 87; DB 4; Ler
Best Local Similarity 43.6%; Pred. No. 1.76e+01;
Matches 17; Conservative 11; Mismatches 6;
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79 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEPYPCPGRR 113
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
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CE 261 AA; 29370 MW; 369384 CN;
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CE 261 AA; 29326 MW; 367179 CN;
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US-08-445-847A-1
                                                                                                                                                01-JAN-1900
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5175255-8
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APPLICANT: MURRAY, MARK J.;KELLY, JAMES D.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOSAIC PROTEINS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,776
FILING DATE: 07-0CT-1994
PRIOR PAPLICATION NUMBER: 926,149
FILING DATE: 05-AUG-1992
APPLICATION NUMBER: 379,239
CFILING DATE: 11-ULL-1899
APPLICATION NUMBER: 941,970
FILING DATE: 3-AUG-1986
APPLICATION NUMBER: 866,485
FILING DATE: 3-AUG-1986
APPLICATION NUMBER: 705,175
FILING DATE: 25-FEB-1986
APPLICATION NUMBER: 706,175
FILING DATE: 12-OCT-1984
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Pred. No. 1.49e+01;
4; Mismatches 1; Indels
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Pred. No. 1.76e+01;
11; Mismatches 6; Indels
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 LQRLLQGDSGKEDGAELDLNMTRSHSGGELESLA-RGKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA.
                                                            APPLICATION NUMBER: US/08/236,918A FILING DATE: 06-May-1994 CLASSIFICATION: 435
                                                                                                                                                                                       NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REPERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFRA: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                          APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE 254 AA; 26624 MW; 316872 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA; 27563 MW; 324570 CN;
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                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       : 254 amino acids
amino acid
                                                                         FILING DATE: 06-May-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Best Local Similarity 66.7%;
Matches 12; Conservative
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Best Local Similarity 43.6%;
Matches 17; Conservative
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US-08-299-567-5
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                                                                                   Score 85; DB 3; Length 613;
Pred. No. 2.44e+01;
13; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85; DB 2; Length 613;
Pred. No. 2.44e+01;
13; Mismatches 18; Indels
                                                                                                                                   1 MRAPGALLARMSRLLLLLLLKVSASSALGVAPASRNETCLGESCA 45
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Endothelin Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325800-322 (PF137)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,687A
FILING DATE: 6 JUNE 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11843
FILING DATE: 17 OCT 1994
ATTORNEY/AGENT INFORMATION:
                      STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
JENCE 613 AA; 67034 MW; 1960405 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ENCE 613 AA; 67034 MW; 1960405 CN;
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08465687A
Patent No. 5750370
                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08465687A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 2:
: 613 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 613 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                              STANDARD;
                                                                                   Query Match
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.9%;
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW JERSEY
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ROSELAND
STATE: NEW JERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07068
                                                                                                                                                                                                           US-08-465-687A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
 LENGIH:
                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 CHLHYEVLLAGLGGSEQGTVT-A-HLLGPPGTPGP-RRLLKGFYGSEAQGVV 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 CRL-YE-LLHGAGNHAAGILTIGKRRPGPPGLQGRLQRLLQA-NGNHAAGIL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.9%; Score 85; DB 2; L
Best Local Similarity 40.4%; Pred. No. 2.44e+01;
Matches 21; Conservative 9; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RACIE, Lisa
APPLICANT: LaVALLIE, Edward
APPLICANT: DeROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
WUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Genetics Institute, Inc. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/749,169A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FENCE 954 AA; 101960 MW; 4424673 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                             Sequence 3, Application US/08749169A
Patent No. 5846770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08299567 Patent No. 5747033 GENERAL INFORMATION:
                                                                                                                                                                                                          Sequence 3, Application US/08749169A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAGAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI STELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08299567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 954 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
RESULT 13

AC XXXXX

AC XXXXXX

DT XX Sequence 3, Applic XX

XX Sequence 3, Applic C C CENERAL INFORMAT E APPLICANT: RACC C CORRESPONDENCE C CORRESPONDENCE C CORRESPONDENCE C CONTRY: MASS.

CC CONTRESPONDENCE C CONTRY: MASS.

CC CONTRY: ASS.

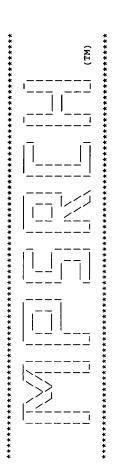
CC CONTRY: MASS.

CC 
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APPLICANT: Davis, et al.

1 MRAPGALLARMSRLLLLLLKVSASSALGVAPASRNETCLGESCA 45



protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:06:48 1999; MasPar time 3.32 Seconds 280.825 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-8

(1-33) from USO8938548B.pep 256 1 OPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence: Title:

Scoring table:

PAM 150 Gap 11

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 Post-processing:

summaries

1:swissprot swiss-prot37 Database:

Mean 31.702; Variance 45.079; scale 0.703 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		œ			SUMMARIES		
Result No.	Score	Query	Query Match Length	DB	ID	Description	Pred. No.
-	75	29.3	373	н	ICEB_MOUSE	CASPASE-11 PRECURSOR (	5.93e-02
N	73	28.5	260	Н	NMA_HUMAN	PUTATIVE TRANSMEMBRANE	1.38e-01
m	72	28.1	815	<del>, -</del>	GYRB_MYXXA	DNA GYRASE SUBUNIT B (	2.10e-01
=#	71	27.7	413	~	PPAW_CAEEL	PUTATIVE ACID PHOSPHAT	3.18e-01
ın	70	27.3	214	Н	R10A_TRYBR	60S RIBOSOMAL PROTEIN	4.80e-01
w	69	27.0	197	~	MCS_MOUSE	SPERM MITOCHONDRIAL CA	7.21e-01
7	69	27.0	461	+-4	YUL2 CAEEL	PUTATIVE FORKHEAD-RELA	7.21e-01
8	89	26.6	641	Н	TETS_LISMO	TETRACYCLINE RESISTANC	1.08e+00
σ	9	26.6	646	Н	TETS_LACLA	TETRACYCLINE RESISTANC	1.08e+00
0	67	26.2	299	Н	ALC_RABIT	IG ALPHA CHAIN C REGIO	1.61e+00
_	67	26.2	92	Н	RE11_SCHPO	MEIOTIC RECOMBINATION	1.61e+00
~	99	25.8	347	Н	GALE_RAT	UDP-GLUCOSE 4-EPIMERAS	2.38e+00
m	99	25.8	348	Н	GALE_HUMAN	UDP-GLUCOSE 4-EPIMERAS	2.38e+00
-	99	25.8	360	<del>, ,</del>	PURK_PSEAE	PHOSPHORIBOSYLAMINOIMI	2.38e+00
'n	99	25.8	38	Н	LEU3_PHACH	3-ISOPROPYLMALATE DEHY	2.38e+00
G	99	25.8	425	~	IFI5_MOUSE	INTERFERON-ACTIVATABLE	2.38e+00
7	65	25.4	15	-	Y115_METJA	HYPOTHETICAL PROTEIN M	3.52e+00
æ	65	25.4	273	Н	MD12_SCHPO	MITOCHONDRIAL INHERITA	3.52e+00
6	64	25.0	7	-	TX03_AGEAP	OMEGA-AGATOXIN IIIA.	5.17e+00
0	64	25.0	83	~	TX4B_AGEAP	OMEGA-AGATOXIN IVB PRE	5.17e+00
	64	25.0		Н	BOLA_HAEIN	BOLA PROTEIN HOMOLOG.	5.17e+00
~	64	25.0	12	Н	AGSW_VULVU	AGOUTI SWITCH PROTEIN	5.17e+00
~	64	25.0	131	Н	AGSW_MOUSE		5.17e+00

	1.10e+01 1.60e+01 1.60e+01 1.60e+01 1.60e+01 1.60e+01 1.60e+01
He SAAAHESS	MYOSIN HEAVY CHAIN, NO GENE 34 PROTEIN. UREASE ACCESSORY PROTE UREASE ACCESSORY PROTE HYPOTHETICAL PROTEIN K TUBULIN BETA CHAIN. PROP PROTEIN. GLYCINE BETAINE TRANSP DNA REPAIR PROTEIN RAD
AGSW_HUWAN CBAC_ALCSP VPE_VICSA ECSC_BACSU ANGT_MOUSE TET1_ENTFA TETM_STAAU EXBB_HAEDU UNCG_CAEEL NMEI_RAT NMEI_RAT	MYSO_HUMAN VG34_HSVEB URED_KLEPN URED_KLEAE Y129_HUMAN TBB_TRYBR PRPD_SALTY BETP_CORGI RADS_YEAST
	<b>нананан</b> а
132 393 493 633 633 150 1464 1464	1976 160 270 270 406 442 483 595
0.0000000000000000000000000000000000000	24. 24. 23. 23. 23. 23. 23. 23. 23. 23. 23. 23
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22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	000044444 0000000000000000000000000000

### ALIGNMENTS

143; O08735; OV-1997 (REL. 35, CREATED) OV-1997 (REL. 35, LAST SEQUENCE UPDATE) OV-1997 (REL. 35, LAST SEQUENCE UPDATE) OV-1997 (REL. 36, LAST ANNOTATION UPDATE) ASE-11 PRECUENCE (REL. 36, LAST ANNOTATION UPDATE) ASE-12 PRECUENCE (REL. 36, LAST ANNOTATION UPDATE) ASE-13 OR CASED. AND ASE-13 OR CASED. AND ASE-14 PRECUENCE (REL. 36, LAST ANNOTATION UPDATE) AND ASE-14 PRECUENCE (REL. 36, LAST ANNOTATION UPDATE) AND ASE-14 PRECUENCE (REL. 36, LAST ANNOTATION UPDATE) AND ASE-14 PRECUENCE (REL. 36, LAST AND UPDATE) ASE-14 ASE-
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EMBL; U34620; G1123023; -. PROSITE; PS01199; RIBOSOMAL_L1; 1. PFAM; PF00687; Ribosomal_L1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selenocysteine codons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
10; Conser
                                                                                                                  214 AA;
                                                                                    RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93039675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCSP OR MCS
                                                                                                                                                                                                                                                                                                                                                                                                                                   MCS_MOUSE
P15265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                  SEQUENCE
                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                              EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                        ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
EL-SARED N.M., DONELSON J.E.;
SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

PROTON DONG (BY SIMILARITY).
BY SIMILARITY.
POLY-GLY.

BE3B5FCE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 71; DB 1; Length 413;
Pred. No. 3.18e-01;
3; Mismatches 7; Indels
                                                                                                                                                                                                              MATTHEWS P.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS -! - CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER
  PUTATIVE ACID PHOSPHATASE C05C10.4 (EC 3.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
60S RIBOSOMAL PROTEIN 110A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WORNPEP, C05C10.4; CE17370.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
PFAM; PF00328; acid_phosphat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 314 PR
381 387 BY
55 60 PO
413 AA; 46617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPANOSOMA BRUCEI RHODESIENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 PDQCAASQNCPCTRYDLLQG 171
                                                                                                                                                                                                                                                                                                                                                                                                                             ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PD-CCROKTCSCRLYELLHG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.7%;
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z48178; E1297507;
                                                      CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL PROTEIN;
                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                       JONES S.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R10A_TRYBR
P53028;
                                                                                                                                                                                                                                                                                                REVISIONS
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ACT_SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90152148.

KLEENE K.C., SMITH J., BOZORGZADEH A., HARRIS M., HAHN L.,
KARIMDOUR I., GERSIEL J.;

Sequence and developmental expression of the mRNA encoding the
seleno-protein of the sperm mitochondrial capsule in the mouse.";

DEV. BIOL. 137:395-402(1990).

-!- FUNCTION: STRUCTURAL PROTEIN OF THE SPERM MITOCHONDRIAL CAPSULE.

IMPORTANT FOR THE MAINTENANCE AND STABILIZATION OF THE CRESCENT
STRUCTURE OF THE SPERM MITOCHONDRIAL.

-!- SUBCELLULAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.

-!- TISSUE SPECIFICITY: TESTIS.

-!- DEVELOPMENTAL STAGE: LATE MEIOTIC AND BARLY HAPLOID CELLS.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KARIMPOUR I., CUTLER M., SHIH D., SMITH J., KLEENE K.C.; "Sequence of the gene encoding the mitochondrial capsule selenoprotein of mouse sperm: identification of three in-phase TGA selenoprometains codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCUUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                            Score 70; DB 1; Length 214; Pred. No. 4.80e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69; DB 1; Length 197; Pred. No. 7.21e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M88463; G459886; -.
EMBL; M29603; G567228; -.
PIR; A37199; A37199.
MGD; MG1:96945; MCS.
MITOCHONDRION; SELENIUM; SPERM; TESTIS; SPERMATOGENESIS.
BINDING 7 SELENIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (REL. 14, CREATED)
01-OCY-1996 (REL. 34, LAST SECUENCE UPDATE)
01-OCY-1997 (REL. 35, LAST ANNOTATION UPDATE)
SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 AA; 21015 MW; 4E56990C CRC32;
24597 MW; EA1B6765 CRC32;
                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELENIUM.
SELENIUM.
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL BIOL. 11:693-699(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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larity 71.4%;
Conservative
                                                                                                                                                                                     52 LPHVCRPRMTVCLLCDLVH 70
                                                                                                                                                                                                                              3 LPDCCRQKTCSCRLYELLH 21
                                                               27.3%;
                                                                                            Local Similarity 42.1%;
                                                                                                                            8; Conservative
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US-08-938-548B-8.rsp

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Region-specific meiotic recombination in Schizosaccharomyces pombe:
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53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X53949; G57792; -. PIR; S11223; S11223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                          EMBL; U70737; G1619901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLGALACTOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALACTOSE 4 - EPIMERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J 12
GALE_RAT
P18645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        MEIOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIS IMMUNOCLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY CHAIN HAPLOTYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNIGHT K.L., MARTENS C.L., STOKLOSA C.M., SCHNEIDERMAN R.D.;
"Genes encoding alpha-heavy chains of rabbit IgA: characterization of
cDNA encoding IgA-g subclass alpha-chains.";
NUCLEIC ACIDS RES. 12.1657-1670(1981 RS. 12.1657-1670(1981 MA)
-!- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
SECRETIONS. IT MAY SERVE BOTH TO DEFEND ACAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                         IG ALPHA CHAIN C REGION (FARESTEL).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 1; Length 299;
Pred. No. 1.61e+00;
4; Mismatches 2; Indels
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594CED7C CRC32;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                                                       21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
1G ALPHA CHAIN C REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE; 97231330.
LI Y.F., NUMATA M., WAHLS W.P., SMITH G.R.;
Mismatches
                                                                                                                                                                                                                                       299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   923 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                       PRT;
2
                                                         SCSLYPVYHGSAKNNIGIKQL 235
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                                                                                          || || : ||:::: || |
SCRLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00290; IG_MHC; 2. PFAM; PF00047; ig; 2. IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
Conservative
                                                                                                                                                                                                                                       STANDARD;
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2 PLPDCCRQKTC-SC 14
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RE11_SCHPO
Q92380;
                                                                                                                                                                                                   LT 10
ALC_RABIT
P01879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                         215
                                                                                                               13
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZESCHNIGK M., WILCKEN-BERGMANN B., STARZINSKI-POWITZ A.; "CDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli."; NUCLEIC ACIDS RES. 18:5289-5289(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIMERIZATION OF UDP-GLUCOSE TO UDP-GALACTOSE AND THE EPIMERIZATION OF UDP-GLUCOSE TO UDP-GALACTOSE AND THE EPIMERIZATION OF UDP-N-ACETYLGLUCOSAMINE TO UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: GALACTOSE METABOLISM.
-i- SIMILARITY: WITH OTHER GALACTOWALDENASES FROM EUKARYOTIC AND PROKARYOTIC ORIGIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66; DB 1; Length 347; Pred. No. 2.38e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 1; Length 923;
Pred. No. 1.61e+00;
6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: UDP-GLUCOSE = UDP-GALACTOSE -!- COFACTOR: NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                          923 AA; 107418 MW; B51C7725 CRC32;
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3EC2E611 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 AA
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PFAM. PF00106; adh_short; 1.
HSSP; P09147; IVVS.
ISOMERASE; NAD; GALACTOSE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the rec11 gene.";
MOL. MICROBIOL. 23:869-878(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.7%;
Matches 10; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A ZAPANTA L.S., HATTORI T., RZETSKAYA M., TIEN M.;
A ZAPANTA L.S., HATTORI T., RZETSKAYA M., TIEN M.;
TCIONING Of PHARAFOCHAEL CHYSOSPOXUM 1802 by complementation of bacterial auxotrophs and transformation of fungal auxotrophs.";
L APPL. ENVIRON. MICROBIOL. 64:2624-2629(1998).
-!- CATANTYIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE +
NAD(+) = 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRODUCT
C DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
C -!- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
C -!- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
C -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
C -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
C -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
                                                                                                                              15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85) (BETA-IPM DEHYDROGENASE)
(IMDH) (3-IPM-DH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; FUNGI; BASIDIOMYCOTA; HYMENOMYCETES; STEREALES;
CORTICIACEAE; PHANEROCHAETE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF050668; G2935579; -.
PROSITE; PS00470; IDH_IMDH; 1.
OXIDOREDUCTASE; LEUCINE BIOSYNTHESIS; NAD.
SEQUENCE 380 AA; 40642 MW; 2645DEB6 CRC32;
                                                      380 AA.
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                                                      PRT;
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                                                      STANDARD;
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SEQUENCE FROM N.A.
STRAIN=ME446;
                                             LEU3_PHACH
059930;
RESULT SOLUTION OF SOLUTION OF
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Search completed: Fri Aug 20 21:07:07 1999 Job time : 19 secs.

1 QPL-PDCCRQKTCSCRLYELLHGAGNHAAG 29

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

MasPar time 5.02 Seconds 263.383 Million cell updates/sec Fri Aug 20 21:06:09 1999; Run on:

Tabular output not generated.

>US-08-938-548B-8 (1-33) from US08938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGILTL 33 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:pirl 2:pir2 3:pir3 4:pir4 pir60 Database:

Mean 30.710; Variance 49.199; scale 0.624 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	3.46e-03	6.20e-01	1.32e+00	1.91e+00	1.91e+00	1.91e+00	2.76e+00	3.98e+00	3.98e+00	5.71e+00	5.71e+00	5.71e+00	8.17e+00	8.17e+00	8.17e+00	8.17e+00	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01
Description	hypothetical protein			oct2 protein isoform	sperm mitochondrial c	hypothetical protein	tetracycline-minocycl	Ig alpha chain C regi	Ig alpha chain C regi	두	gene D3 protein - mou	transcription regulat	conserved hypothetica	keratin KAP5.5 - shee	beta-fructofuranosida	hypothetical protein	omega-agatoxin IVB -		omega-agatoxin III, 8	omega-agatoxin IIIA -	cell division protein	pigment deposition co	agouti protein precur
DI	T00728	S24303	A41130	860079	A37199	T01864	JN0800	AHRB	S09276	S11223	I56329	B69764	C64314	146413	833920	T01164	A44664	A54252	B54252	A42335	B64052	A46298	137143
DB	2	7	7	~	7	~	~	-	~	7	7	7	~	7	7	7	Н	7	7	~	7	7	7
Length	915	147	870	93	143	533	641	299	338	347	425	479	155	197	589	806	48	9/	9/	9/	103	131	132
% Ouery Match	33.2	28.1	27.3	27.0	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0
Score	85	72	70	69	69	69	68	29	29	99	99	99	65	65	65	65	. 64	64	64	64	64	64	64
Result No.	1	7	ю	4	5	9	7	ω		10	11	12	13	14	15		17	18	19	20	21	22	23

25.0 369 2 B64835 probable iron-sulfur- 1.16e+01 24.6 236 2 49975 cysteine proteinase ( 1.16e+01 24.6 236 2 809271 Ig alpha chain C regi 1.65e+01 24.6 360 2 809271 Ig alpha chain C regi 1.65e+01 24.6 577 2 A2978 amjotensin precursor 1.65e+01 24.6 537 2 701052 heatshock protein dna 1.65e+01 24.6 639 2 A50633 tetracycline resistan 1.65e+01 24.6 639 2 A50779 tetracycline resistan 1.65e+01 24.2 138 2 G70431 hypothetical protein 2.33e+01 24.2 157 2 JH0799 laminin-related prote 2.33e+01 24.2 157 2 JH0799 laminin-related prote 2.33e+01 24.2 1464 2 A43274 N-methyl D-aspartate 2.33e+01 24.2 1464 2 S29159 glutamate receptor, N 2.33e+01 25.8 1169 1 S64859 DNA repair protein - equ 3.28e+01 25.8 1169 1 S64859 myosin heavy chain-B, 3.28e+01	T00728 hypothet #formal_cress 12-Feb-1 10728 2140000 Shinn, P Sun, H Y.K.; Feders submitte Genomic T00728 Ltype Dre Ltype Dre Ltype Dre 1 1-9	tch 33.2%; Score 85; DB 2; Length 915; al Similarity 61.5%; Pred. No. 3.46e-03; 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0; ERTCSCRAPDLLH 806 ::
. 2224 22554 2276554 22776554 2377655 24776 24776 247765 24776 24776 24776 247765 247765 247765 247765 247765 247765 247765 2477	RESULT 1 EMTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #submission #submission #status ##status ##residues ##residues ##residues ##residues	Query Match Best Local Simila Matches 8; 6 Db 794 ERTCSCRAL OY 9 OKTCSCRL OY 9 OKTCSCRL TITLE BREY TITLE BACCESSIONS STREFERENCE STREFEREN

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#cross-references MUID:90384840
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ALTERNATE_NAMES
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189-261
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##cross-references GB:X00353; NID:g1575; PID:g1576
IT This immunoglobulin belongs to the IgA-g subclass. It was isolated
from a rabbit homozygous for a2, n80, de12,15, f71, g75 heavy
chain haplotype.
                                                                                                                                                                                                                                                                                                                                                                                        the start codon is "TTG" encoding a "Leu" amino acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                               #authors Charpentier, E.; Gerbaud, G.; Courvalin, P.
#journal Gene (1993) 131:27-34
#title Characterization of a new class of tetracycline-resistance
gene tet(S) in Listeria monocytogenes BM4210.
#cross-references MUID:93380670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knight, K.L.; Martens, C.L.; Stoklosa, C.M.; Schneiderman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily translation elongation factor G; translation
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                                                                    tetracycline-minocycline resistance protein - Listeria monocytogenes (strain BMA10) plasmid pIPB11 formal_name Listeria monocytogenes 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
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#length 641 #molecular-weight 73013 #checksum 8738
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characterization of cDNA encoding IgA-g subclass
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#region nucleotide-binding motif A (P-loop)\
#region GTP-binding NKXD motif\
#region GTP-binding SAK/L motif\
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##experimental_source strain BM4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elongation factor Tu homology
antibiotic resistance; GTP binding; P-loop
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Pred. No. 2.76e+00;
5; Mismatches 7
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                                                     #type complete
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##residues 1-641 ##label CHA
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                                                                                                                                                                                                                                                                                                                                                                                                           the paper
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Best Local Similarity 42.9%;
Matches 9; Conservative
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*superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin; plasma
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Nucleic Acids Res. (1990) 18:5289
cDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alipha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.; Starzinski-Powitz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S09276 #type fragment
If alpha chain C region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S11223 #type complete
UDPglucose 4-epimerase (EC 5.1.3.2) - rat
UDPgalactose 4-epimerase recomment and the state of the st
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16-Aug-1996
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The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
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#length 338 #checksum 2169
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Pred. No. 3.98e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.2%;
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.2%;
Similarity 50.0%;
7; Conservative
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PLPDCCRQKTC-SC 14
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Best Local Similarity
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533920

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#gene
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KEYWORDS
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beta-fructofuranosidase (EC 3.2.1.26) precursor - Aspergillus
                                                                                                                                                                                              #superfamily Methanococcus jannaschii conserved hypothetical protein MJ0115 #length 155 #molecular-weight 17727 #checksum 834
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#title Differential expression of genes encoding a cysteine-rich keratin family in the hair cuticle.
#cross-references WUID:94358466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Boddy, L.M.; Berges, T.; Barreau, C.; Vainstein, M.H.;
Dobson, M.J.; Ballance, D.J.; Peberdy, J.F.
#journal Curr. Genet. (1993) 24:60-66
#title Purification and characterisation of an Aspergillus niger
#cross-references MUID:93365038
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             keratin KAPS.5 - sheep (fragment)

#formal_name Ovis orientalis aries, Ovis ammon aries

#common_name domestic sheep
16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
13-Sep-1998
833920; 836775
                                                        preliminary; nucleic acid sequence not shown; translation not shown
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##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-197 ##label JEN
##cross-references EMBL:X73435; NID:9313721; PID:9313722
                                                                                                                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                                                                                                   4; Indels
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Pred. No. 8:17e+00;
2; Mismatches 3; Indels
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#superfamily ultra-high-sulfur keratin
#length 197 #checksum 2787
                                                                                                                                                                                                                                         #molecular-weight 17727
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Pred. No. 8.17e+00;
2; Mismatches 4
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Methanococcus jannaschii. #cross-references MUID:96337999
                                                                                                                                                 TIGR: MJ0115
                                                                                                                                                                                    #map_position REV113249-112782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                     72 CCKITKPCPYRDYEL 86
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                                                                                          ##molecule_type DNA
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##molecule_type DNA
##residues
1-589 ##label BOD1
##ccession
536775
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##molecule_type protein
##residues
24-35,79-92;369-383;402-413 ##label BOD2

CLASSIFICATION
##superfamily beta-fructofuranosidase
##concession
##residues

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GENETICS

CLASSIFICATION
##superfamily beta-fructofuranosidase
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:08:23 1999; MasPar time 1.89 Seconds 176.899 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-8 (1-33) from USO8938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33

Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

106580 seqs, 10152877 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Mean 21.693; Variance 81.714; scale 0.265

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	4.41e+01	5.37e+01	5.37e+01	5.37e+01	7.93e+01	7.93e+01	9.63e+01	9.63e+01	9.63e+01	9.63e+01	9.63e+01	1.17e+02	1.17e+02	1.41e+02
Description	Sequence 40, Applicati	40,	40,		40,	40,	40,		2, A	20,	6, 4	9	6	11,	Sequence 1, Applicatio	23,		23,	Sequence 23, Applicati	51,	52	Sequence 10, Applicati	Sequence 2, Applicatio
DI	PCT-US95-0	US-08-249-	US-08-734-	US-08-469-	US-08-036-	PCT-US94-0	US-08-469-	US-08-469-	PCT-US95-0	US-08-469-	US-08-485-	ns-08-200-	US-08-620-	US-08-231-	US-08-026-	US-08-137-	US-08-487-	US-08-477-	US-08-480-	US-08-233-	5223425-6	-2	us-08-658-
DB	m	Н	7	7	Н	r	Н	7	m	~	Н	N	-	a	Н	-	Н	Н	<del>, ,</del>	Н	4	Н	-
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% Query Match			25.8		25.8		٠	25.8	25.8	25.4	25.0	25.0	'n	₹.		Э.	m	23.8		23.8	23.4	23.4	23.0
Score	99	99	99	99	99	99	99	99	99	65	64	64	64	62	62	61	61	61	61	61	09	09	29
Result No.	1	7	æ	4	Ŋ	Q	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.41e+02 1.41e+02 1.41e+02 1.71e+02 1.71e+02 1.71e+02 1.71e+02 2.07e+				ni, Mark;
Sequence 4, Application Sequence 2, Application Sequence 2, Application Sequence 10, Application Sequence 11, Application Sequence 11, Application Sequence 5, Application Sequence 6, Application Sequence 11, Application Sequence 2, Application Sequence 3, Application Sequence 3, Application Sequence 13, Application Sequence	S	PRI; 39 AA.	46A	846A. id: Stroobant, Paul; terfield, Michael; Marchioni, '. Ian enic Factors, Their and Use  12. 12. 13. 19. 19.
1 US-08-296- 1 US-08-296- 1 US-08-296- 2 US-08-757- 2 US-08-757- 2 US-08-757- 2 US-08-757- 2 US-08-757- 2 US-08-757- 2 US-08-757- 2 US-08-951- 2 US-08-951- 2 US-08-951- 3	ALIGNMENT	STANDARD;	n PC/TUS9506846A	Sequence 40, Application PC/TUS9500846A GENERAL INFORMATION: APPLICANT: Goodearl, Andrew David; Stroot APPLICANT: Chen, Maio Su; Hiles, Ian TITLE OF INVENTION: Glial Mitogenic Facto TITLE OF INVENTION: Glial Mitogenic Facto TITLE OF SEQUENCES: 178 CORRESPONDENCE ADDRESS: ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York CITY STREET: 805 Third Avenue CITY: New York CITY CONFUTE: New York CITY STREET: New York CITY COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 k SOFTWARRE: Wordperfect COMPUTER: 1BM OPERATION NUMBER: 07/965,173 FILING DATE: 24-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/940,389 FILING DATE: 33-CCT 1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/940,389 FILING DATE: 03-SEP-1992 PRIOR APPLICATION DATA: APPLICA
0 1019 0 1019 1083 1 131 1 131 1 132 3 3 424 3 424 3 424 3 720 3 1184 3 1184 3 1187 3 1187		A-40	Application	quence 40, Application FC, BNERAL INFORMATION: BAPLICANT: Chen, Maio St APPLICANT: Chen, Maio St TITLE OF INVENTION: Polit CORRESPONDENCE ADDRESS: ADDRESSE: Felfe & LYSTREET: 805 Third Aver CITY: New York COUNTR: DAS FELF FORM: WOOFFICE OF FILLING DATE: 26-MAY-19 PRIOR APPLICATION NUMBER: OF FILLING DATE: 24-MAR-19 PRIOR APPLICATION NUMBER: OF FILLING DATE: 24-MAR-19 PRIOR APPLICATION NUMBER: OF FILLING DATE: 24-MAR-19 PRIOR APPLICATION NUMBER: OF FILLING DATE: 34-MAR-19 PRIOR APPLICATION NUMBER: OF FILLING DATE: 34-MAR-19 PRIOR APPLICATION NUMBER: OF FILLING DATE: 35-SEP-19 PRIOR APPLICATION DATA: APPLICATION NUMBER: OF FILLING DATE: 35-SEP-19 PRIOR APPLICATION DATA: APPLICATION NUMBER: OF PRIOR APPLICATION DATA: APPLICATION DA
		-06846A-40	40, 8	ce 40, Appl. ce 10, Cont. ce 40, Appl. ce 111CANT: Ch. ce 40, Appl. ce 111CANT: Ch. ce 40, Appl. ce 111CANT: Ch. ce 40, Appl. ce 40, Ap
50000000000000000000000000000000000000	н	PCT-US95- XXXXXX	Sequence	Sequence GENERAL APPLII APPLII APPLII TITLE TITLE TITLE TITLE CORR CORR COM
00000000000000000000000000000000000000	SUL			##888888888888888888888888888888888888

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Sequence 40, Application US/0803555B
Patent No. 5530109
GENERAL INFORMATION:
APPLICANT: Geodearl, Andrew; Stroobant, Paul;
APPLICANT: Geodearl, Andrew; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 AA
                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/01,396
FILING DATE: 29-JAN-1993
APPLICATION DATA:
APPLICATION NUMBER: 07/984,085
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747
FILING DATE: 10-AUG-1992
ATONNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555B
FILING DATE: 24-MAR-1993
                         US/08/469,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40, Application US/08036555B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGY: linear
39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.8%;
Best Local Similarity 70.0%;
                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CCR-TICACR 16
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ID US-08-036-555B-40
                                           FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Patent No. 5876973
GBNERAL INFORMATION:
APPLICANT: GWYDNE, David I.; Marchionni, Mark;
APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
TIP: 0211-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AA.
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Pred. No. 3.62e+01;
                                                                                                                                                                                                                                                                                                                                  TORNEY/AGENT INFORMATION.
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REGISTRATION NUMBER: 04585/00200P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
APPLICATION NUMBER: 08/470,335
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 03-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION NUMBER: 07/963,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION NUMBER: 07/966,389
FILING DATE: 03-APR-1992
PRIOR APPLICATION NUMBER: 07/967,138
FILING DATE: 03-APR-1992
PRIOR APPLICATION NUMBER: 07/967,138
FILING DATE: 10-APR-1992
ATTORNEY AMENT INFORMATION
NUMBER: 10-APR-1991
ATTORNEY AMENT INFORMATION
NUMBER: 10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MELLU...
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 39
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GENERAL INFORMATION:
APPLICANT: JI,H, ET AL.
TITLE OF INVENTION: HUMAN UDP GALACTOSE-4-EPIMERASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDERS:
ADDRESSE: CARCHIA, BYRNE, BAIN, GILFILLAN,
ADDRESSE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length 39;
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Pred. No. 3.62e+01;
1; Mismatches 1
                                 FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 03-JUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APPLI-1992
APPLICATION NUMBER: 07.866.3
FILING DATE: 10-APR-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                    NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0578
Sequence 2, Application PC/TUS9505785
                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NCE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
RESISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Concurrently
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CCR-TTCACR 16
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PCT-US95-05785-2
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APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Warchionni, Mark
APPLICANT: Chen, Maio Su
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 1; Length 39;
Pred. No. 3.62e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,526A
FILING DATE: 06 June 1995
CLASSTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 AA.
                                                            APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
RIOR APPLICATION DATA: 1992
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTONEN/AGENT INFORMATION:
NAME: TSai, Christine H.
REGISTATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 5250.4
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application US/08469526A Patent No. 5792849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/08469526A
                      APPLICATION NUMBER: 07/907,138
                                                                                                                                                                                                                                                                                                                                   39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodearl, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                     30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                  FILING DATE: 30-JUN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                        linear
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringiensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0%; Score 64; DB 2; Length 1167
Best Local Similarity 45.5%; Pred. No. 5.37e+01;
Matches 5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Galnesville STATE: Florida COUNTRY: USA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,053
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: SALIWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
RREFERENCE/POCKET NUMBER: 31,794
REFERENCE/POCKET N
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08620717A Patent No. 5670365 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08620717A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-0CT-1995
N: 435
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   873 PNCCKPAACQC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PDCCROKTCSC 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-620-717A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08590554A
Patent No. 583101
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Narva, Kenneth E.
APPLICANT: Narva, Genry M.
APPLICANT: Fu, Jenny M.
APPLICANT: Pu, Jenny M.
APPLICANT: Pu, Jenny M.
APPLICANT: Pu, Senneth E.
APPLICANT: Pu, Senneth E.
APPLICANT: Pu, Jenny M.
TITLE OF INVENTION: No. 5831011el Bacillus thuringiensis Genes Encoding TITLE OF INVENTION: No. 58310161el Bacillus thuringiensis Genes Encoding NUMBER OF SEQUENCES:
ADDRESSEE: David R. Saliwanchik
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                                                                                                                                                                                                                  Length 1167;
                                                                                                                                                                                                                Score 64; DB 1; Length 1167
Pred. No. 5.37e+01;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,554A
FILING DATE: 21-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,568
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,197
FILING DATE: 21-SEP-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                              1167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/918,345 FILING DATE: 21-JUL-1992 CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/357,698
FILING DATE: 16-DEC-1994
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APPLICATION NUMBER: US 07/558,738
FILING DATE: 27-JUL-1990
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08590554A
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
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Best Local Similarity 45.5%;
Matches 5; Conservative
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US-08-590-554A-6
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Gaps

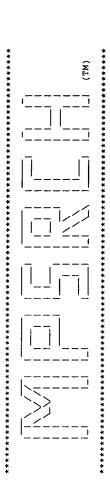
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ö Ouery Match
24.2%; Score 62; DB 1; Length 1464;
Best Local Similarity 23.3%; Pred. No. 7.93e+01;
Matches 7; Conservative 11; Mismatches 12; Indels 0; Gaps CC RELEVANT RESIDUES IN SEQ 1D NO: 1: FROM 1 to 1464 SQ SEQUENCE 1464 AA; 165489 MW; 11224000 CN;

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QQ

Search completed: Fri Aug 20 21:08:30 1999 Job time : 7 secs.



protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:05:04 1999; MasPar time 5.22 Seconds 134.533 Million cell updates/sec Run on:

Tabular output not generated.

(1-33) from USO8938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 >US-08-938-548B-8 Description: Perfect Score:

Scoring table:

Sequence:

PAM 150 Gap 11

170751 seqs, 21266608 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part8 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part11 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Variance 84.044; scale 0.274 Mean 23.069; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ø					
Result No.	Score	Query Match	° Query Match Length DB	DB	£ £	Description	Pred. No.
-	256	100.0	123	33	W61383	Mouse HFGAN72 recepto	1 859-18
7	. 256	100.0	130	30	W50158	Mouse hypocretin 35.	1.85e-18
m	256	100.0	130	33	W61382	Rat HFGAN72 receptor	1.85e-18
4	256	100.0	130	30	W50157	Rat hypocretin 35.	1.85e-18
ស	256	100.0	131	33	W61381	Human HFGAN72 recepto	1.85e-18
9	77	30.1	363	23	W12414	Porcine complement in	8.08e+00
7	7.5	29.3	373	31	W56031	Mouse ICH-3.	1.22e+01
ω	75	29.3	373	13	R66767	Murine interleukin-1	1.22e+01
თ	75	29.3	373	18	R98461	Murine ICE-ced-3 homo	1.22e+01
10	73	28.5	1876	29	W38757	Phosphatidyl inositol	1.85e+01
11	69	27.0	329	56	W29877	Lysophosphatidic acid	4.19e+01
12	99	25.8	102	,-	P95679	Xenopus Vq1 protein f	7.64e+01
13	99	25.8	348	21	W01619	Human uridine diphosp	7.64e+01
14	65	25.4	14	30	W52512	Cyclic peptide of the	9.31e+01
15	65	25.4	78	S	P20020	Sequence of a foot an	9.31e+01
16	65	25.4	92	30	W53894	Fragment of chimeric	9.31e+01

antibodies, antagonists, etc.

Claim 5; Fig 5; 35pp; English.

The HFGAN72 receptor protein contains two ligans whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGAN2 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral nifections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, Parkinson's disease, both acute and congestive heart failure,

hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign

9.31e+01 1.13e+02 1.1
Human 7-transmembrane Murine agouti signalli AGI toxin. Calcium channel inhib A. aperta venom fract Human agouti signalli Mouse agouti protein. Murine agouti protein. Murine agouti signalli Mouse agouti protein. Murine agouti signalli Protein encoded by ag Nematocidal toxin 167P pacillus thuringiensi Nematocidal toxin 167P pacillus thuringiensi Nematocidal toxin 167P pacillus thuringiensi Nematocidal protein of the specif Human N-methyl-D-aspa Human N-methyl-D-aspa Glutamic acid recepto Human NDA R2A receptor Rat NMDA receptor sub A-lineage conotoxin predatory cone sanil Human membrane antige TctA sequence. Ehrlichia sp. extende Human by protein asso
W62598 W10105 W10105 W10106 R45611 R60293 W10102 W10102 W10101 W16326 W10653 W16326 W16326 W16326 W16326 W16326 W16326 W16339 W1
66 88 88 88 88 88 88 88 88 88 88 88 88 8
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#### ALIGNMENTS

Mouse HFGAN72 receptor protein.
HFGAN72 receptor exting disorders; renal disease; heart failure;
HFGAN72 receptor; eating disorders; renal disease; heart failure;
exual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder. (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI; 98-334672/29. HFGAN72 receptor ligands - and corresponding DNA, agonists, 33..65 /note= "Ligand 72A" 69..96 /note= "Ligand 72B" Location/Qualifiers standard; Protein; 123 AA (first entry) 24-JUN-1998. 17-DEC-1997; 310216. 26-SEP-1997; US-933093. 17-DEC-1996; US-820504. 19-MAR-1997; US-820519. 02-JUL-1997; US-887382. EP-849361-A2 02-OCT-1998 W61383; W61383 Mus sp Region Region  US-08-938-548B-8.rag

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HFGAN72 (zeceptor protein. HFGAN72 receptor; eating disorders; renal disease; heart failure; HFGAN72 receptor; eating disorders; renal disease; heart failure; excual dysfunction; HIV; cancer; Parkinson's disease; urinary retention; osteoporosis; angina pectoris; myocardial infarction; psychotic disorder; neurological disorder.
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                                                                                                                                                                                                                                                                                                   Gaps
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect
                                                   the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor.
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                                                                                                                                                                                                                                         Length 130;
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(SMIK ) SMITHKLINE BEECHAM PLC.

(SMIK ) SMITHKLINE BEECHAM PLC.

BEGSGRM DJ, BLOOKS DP, Gellai M, Wilson S, Yanagisawa M;

WPI; 98-324672/29.

N-PSDB; V28138.

HFGAN72 receptor ligands - and corresponding DNA, agonists,
                                                                                                                                                                                                        Score 256; DB 30; Length Lovered. No. 1.85e-18;
                                                                                                                                                                                                                                                                                                                                                         33 qplpdccrqktcscrlyellhgagnhaagiltl 65
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/note= "Ligand 72A"
70..97
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/note= "Ligand 72B"
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Claim 2; Fig 2; 35pp; English.
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Local Similarity 100.0%;
nes 33; Conservative
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Local Similarity 100.0%;
nes 33; Conservative
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26-SEP-1997; US-938093.
17-DEC-1996; US-038604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
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Transgenic knock-out mice containing new Ich-3 disrupted generates yes an experient to a screening for compounds to treat septic shock and defects in folliculogenesis.

Transgenic knock-out mice compounds to treat septic shock and defects in folliculogenesis.

Example 1, Page 67.4-67.5; 99pp; English.

The present invention describes: (1) a method for modulating programmed cell death in a cell, comprising contacting the cell with modulating amounts of ICH-3; (2) a method for promoting pro-interleukin (pro-IL) (ICE), comprising contacting the cell with ICH-3 expressed under the control of a CMV promoter; (3) a method for stimulating synthesis of Ich-3 gene products in a cell, comprising contacting the cell with contacting the cell with contacting the cell with stimulatory amounts of lipopolysaccharide (ICE); (GES); (4) a monoclonal or polyclonal antibody that specifically binds to ICH-3; (5) a transgenic non-human animal, comprising a disrupted ICH-3 gene, and its progeny,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This protein is a porcine complement inhibitor encoded by pMCPcDNA (T61098). The DNA is useful for large scale production of recombinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pWCPcDNA is also useful in the analysis of the promoter region of porcine complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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                                                                W12414;
24-SEP-1997 (first entry)
Porcine complement inhibitor.
porcine; pig; complement; inhibitor; organ transplantation;
analysis; promoter.
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Pred. No. 8.08e+00;
"..matrhes 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murakami H, Shigehisa T, Toyomura K;
WPI; 97-087378/08.
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WPI; 98-159183/14.
N-PSDB; V28526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplant to humans
Claim 3; Page 12-14; 20pp; Japanese.
                                    W12414 standard; Protein; 363 AA.
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39.38;
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28-JUL-1998 (first entry)
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09-AUG-1996; US-023937.
(FISH/) FISHMAN J A.
                                                                                                                                                                                                                                                                                                                                                                       09-JAN-1997.
19-JUN-1996; J01704.
20-JUN-1995; JP-178254
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Matches 11; Conserv
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(WANG/) WANG S.
(YUAN/) YUAN J.
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WO9700951-A1.
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WO9806263-Al.
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34 qplpdccrqktcscrlyellhgagnhaagiltl 66 1. QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 S

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a novel mammalian lysophosphatidic acid acyltransferase (LPAAT) enzyme, designated LPAAT I. Enzymes LPAAT I. LPAAT II. ac human homologues of non mammalian forms of LPAAT. The sequences can be used to screen for LPAAT inhibitors and to study the role of LPAAT enzymes in signal transduction and disease. note: the present sequence does not appear in the specification; it was sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1990 (first entry)
Xenopus Vg1 protein for osteogenic device.
Osteogenic device; osteogenic protein; endochronal bone; biodegradable
                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1998 (first entry)
Lysophosphatidic acid acyltransferase enzyme LPAAT I splice variant 1.
Lysophosphatidic acid acyl transferase; LPAAT; mammalian;
LPAAT inhibitor; signal transduction.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian lyso-phosphatidic acid acyl-transferase enzymes - and related DNA, useful for isolating inhibitors and studying the role of the enzymes in signal transduction Disclosure; Page -; 5pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteogenic devices comprising matrix contg. osteogenic proteins prepd. by recombinant techniques.
Claim 7: page 48: 69pp: English.
The protein is capable of inducing endochronal bone formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                Indels
Pred. No. 1.85e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                        501 rrktct-rlyelisdgrtddpell 523
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P95679:
                                                                                                                                                        W29877 standard; Protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STAM/) STAMPS A.
(YAMA-) YAMANOUCHI RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.0%;
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                             Best Local Similarity 41.7%;
                                                                10; Conservative
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20-7UL-1997; RD-400054.
(ELMO/) FLNNEN M A.
(FINN/) FINNEN M J.
(HILL/) HILL M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
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07-APR-1989; US-179406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dplpgcarh-pcvcr
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07-APR-1989; 901469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KELL/) KELLY K.
(MAKD/) MAKDA A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 89-324203/44.
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WO8909788-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RD-400054-A.
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                                                       Matches
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matrix. The protein is produced by expression of the recombinant DNA in a host cell and comprises more than one polypeptide chain, with an amino acid sequence sufficiently duplicative of COP5, COP7, COP16 or OP1. The protein and the implantable devices enable optimal predictable bone formation. Clinical applications include correction of acquired and congenital craniofacial and other skeletal or dental anomalies, induction of local endochondral bone formation in non-union fractures, peridontal applicant of osteoarthritis.

See also P95679-P95692 and N95097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclic peptide of the invention.

Loop region; cyclic peptide; antimicrobial; disinfectant; therapy;
preservative; amphipathic anti-parallel beta-sheet region; plant disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding human uridine diphosphate galactose-4-epimerase - used in the treatment and diagnosis of galactosaemia claim 1: Page 43-44. 59pp; English.

Claim 1: Page 43-44. 59pp; English.

Claim 1: Page 43-44. 59pp; English.

(W01619) catalyses a reversible reaction between UDP-glucose and UDP-gladactose that allows galactose residues to enter into the main UDP-glucose that allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a cDNA clone (T58301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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Pred. No. 7.64e+01;
....ma+rhes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
association with a biocompatible, in vivo biodegradable
                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 1; Louis Pred. No. 7.64e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W01619 standard; Protein; 348 AA.
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11-MAY-1995; UO5785.
11-MAY-1995; WO-UO5785.
GHUMA-) HUMAN GENOME SCI INC.
Ji H, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                      25.8%; 56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.8%;
53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 CSCRLYELLHGAGNHA 27
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12 CSCRLYELLHGAG 24
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23-JUL-1997; U12974.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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WPI; 96-518666/51.
N-PSDB; T58301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 AA;
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WO9635778-A1.
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WO9803192-Al.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:07:24 1999; MasPar time 6.81 Seconds 264.437 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-8 (1-33) from USO8938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILIL 33 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 30.498; Variance 47.204; scale 0.646 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	1.84e-42	1.84e-42	1.84e-42	1.84e-42	7.54e-02	2.55e-01	3.80e-01	3.80e-01	3.80e-01	3.80e-01	5.64e-01	1.23e+00	1.23e+00	1.23e+00	1.82e+00	1.82e+00	2.66e+00	2.66e+00	2.66e+00	2.66e+00
Description	HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	PREPRO-OREXIN.	PORCINE MEMBRANE COFAC	F14B4.1 PROTEIN.	T05A1.3 PROTEIN.	PHOSPHOINOSITIDE 3-KIN	PHOSPHOINOSITIDE 3-KIN	PHOSPHOINOSITIDE 3-KIN	3' ORF.	SIMILAR TO GALACTOKINA	DYSTROPHIN (FRAGMENT).	DNA POLYMERASE III ALP	SHIKIMATE DEHYDROGENAS	T7M24.1 PROTEIN.	INOSITOL MONOPHOSPHATE	CYCLIN G.	HYPOTHETICAL 78.2 KD P	TYROSINE KINASE.
ID	055241	055232	077668	043612	002839	093473	022187	024209	001938	024453	061639	001969	091493	068770	052422	081510	052736	054779	049426	090975
DB	11	11	9	4	9	Ŋ	ഗ	ഹ	Ŋ	'n	1	Ŋ	13	C)	~	10	7	11	10	13
% Query Match Length	130	130	131	131	363	752	683	1876	1876	1876	147	426	883	1135	163	533	259	293	672	1382
ch	. 0.	0.	0.	0.	30.1	8.9	8.5	8.5	28.5	28.5	28.1	27.3	27.3	27.3	27.0	27.0	9	9	9.9	9
% Query Match	100.0	100.0	100.0	100.0	8	78	58	28	58	58	28	27	27	27	27	27	26	56	56	56
Score	256	256	256	256	77	74	73	73	73	73	72	70	70	70	69	69	68	99	68	9
Result No.		7	e	4	Ŋ	<b>v</b>	7	∞	თ	10	11	12	13	14	15	16	17	18	19	20

3.89e+00	5.666+00	8.20e+00	8.20e+00	8.20e+00	8.20e+00	1.18e + 01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	2.44e+01	2.44e+01
C34B2.7 PROTEIN.	HOMOLOGIF OF REGILATOR	KAP5.5 KERATIN PROTEIN	UL6 AND UL7 GENES, PAR	BETA-D-FRUCTOFURANOSID	F7N22.10 PROTEIN.	COSMID C04E6.	FROM BASES 996879 TO 1	SELENOPHOSPHATE SYNTHE	SELD PROTEIN.	ARYLSULFATASE.	REPRESSOR/INDUCER PROT	COSMID C27A2.	RIBONUCLEASE.	T21B10.6 PROTEIN.	F21C3.1 PROTEIN.	AMINO ACID TRANSPORTER	YUP8H12R.35 PROTEIN.	TETRACYLINE RESISTANCE	ORF11.	LET 858.	SIMILARITY TO EGF-LIKE	METALLOTHIONEIN.	NONMUSCLE MYOSIN HEAVY
044954	P94426	028584	056666	013388	065227	001473	P75863	018597	018373	043113	909500	018238	004393	922627	019671	039135	064546	602790	057224	017336	018857	044127	062706
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67	99	65	65	9	65	64	64	64	64	64	63	63	63	63	63	63	63	63	63	63	63	62	62
21	73	24	25	36	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

OF STATE OF STATE OF STATE STA	01-JUN-1998 (TREMBLREL. 06, CREATED) 01-JUN-1998 (TREMBLREL. 06, IAST SPOTENCE HDDATE)	(TREMBLREL. 08, LAST	CRETIN (PREPRO-OREXIN).		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;	SCIURUGNATHI; MUKIDAE; MUKINAE; MUS.	SEQUENCE FROM N.A.	MEDLINE; 98150861. Saminal t. amemiya a . ishii m. matshami i . Chembili d. m		CARR S.A., ANNAN R.S.,	MCNULIY D.E., LIU WS., TERRETI J.A., ELSHOURBAGY N.A., BERGSMA D.J.,	Indications I., Transition and Travin recenters, a family of hymothalamic neuronestides	G protein-coupled receptors that regulate feeding behavior.";	CELL 92:573-585(1998).		SEQUENCE FROM N.A.		MEDLINE; 98081872.	DE LECEA L., KILDUFF T.S., PEYRON C., GAO XB., FOYE P.E.,	IELSON P.E., FUKUHARA C., BATTENBERG E.L.F., GAUTVIK V.T.,	TLETT F.S. III, FRANKEL F.S., VAN DEN POL A.N., BLOOM F.E.,	GAUTVIR K.M., SUITLIFFE U.S.; THRE PROPORTERING PROPERTY OF THE CONTRACT OF TH		PROC. NATL. ACAD. SCI. U.S.A. 95:322-327(1998).		SEQUENCE FROM N.A.		DE LECEA L., KILDUFF T.S., PEYRON C., GAO XB., FOYE P.E.,	IELSON P.E., FUKUHARA C., BATTENBERG E.L.F., GAUTVIK V.T.,		SAUTVIK K.M., SUTCLIFFE J.G.;		L) APUNICACY COORDING.	AF 013300;	. 1471 . 1771 . 1
RESULT ID 055	010	01-	HYPO	MUS	EOK	17.	SEQ	MED	TAN	ARC	MCN	10	and	CEL	[2]	SEQ	STR	MED	DE	DAN	BAR	0 4 E	act	PRO	[3]	SEO	STR	DE	DAN	BAR	GAU	SUB	CMDL)	MGD	)
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                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                           SEQUENCE FROM N.A.
                         T05A1.3 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                        LLOYD C.;
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Q24209
Q24209;
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WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., KOOPRA A., SAUNDERS D., SHOWNKEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VADION M., VADIGHAN R., WATERSTON R.,
WATENSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.)

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                            Gaps
                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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                                                                 Score 77; DB 6; Length 363;
Pred. No. 7.54e-02;
7; Mismatches 9; Indels
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Pred. No. 2.55e-01;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                       STEWARD C.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                            AD14F57A CRC32;
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                                                                                                                                                                                   752 AA
                                                                                                               98 PLQEACRRKACS-NLPDPLNGQVSYPNG 124
                                                                                                                             2 PLPDCCRQKTCSCRLYELLHGAGNHAAG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, 281078; E1346430; -...
EMBL, 275535; E1346430; JOINED.
EMBL, 275535; E1345510; JOINED.
EMBL, 281078; E1345510; JOINED.
PROSITE; PS01010; ASX_HYDROXYL; PROSITE; PS01187; EGF_CA; 1...
PROSITE; PS01209; LDLRA_1; 2...
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 752 AA; 84505 MW; D060D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q22187 PRELIMINARY; PRT; Q22187; 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                         CREATED)
                                                                                                                                                                                    PRT;
IMMUNOL. 9:869-876(1997).; D70897; D1021310; -.
                                             363 AA; 39692 MW;
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56.3%;
                                                                 Query Match 30.1%;
Best Local Similarity 39.3%;
Matches 11; Conservative
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093473; 093693;

01-FEB-1997 (TREMBLREL. 0

01-NOV-1998 (TREMBLREL. 0

01-AUG-1998 (TREMBLREL. 0

F1484:1 PROTEIN.
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                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
         EMBL; D70897; D1021310
PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                             SEQUENCE
                                   MEMBRANE
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BONFIELD J., BURTON J., CONNELL M., COPER J., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMONE B., O'CALLAGRAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96278830.
MOLZ L.M., CHEN Y.W., HIRANO M., WILLIAMS L.T.;
"Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
domain.";
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                                                                                                                                                             RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                     CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
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EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
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Pred. No. 3.80e-01;
                                                                                                                                                                                                                                                                        SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z68219; E1349116; -.
SEQUENCE 683 AA; 77437 MW; B9B00EA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1876 AA
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PFAM; PF00454; P13 P14_Kinase; 1.

PFAM; PF00613; P13Ka; 1.

PFAM; PF00787; PX; 1.
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01, 1
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50.0%;
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PFAM; PF00794; PI3K_rbd; 1
SEQUENCE 1876 AA; 21050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans.";
NATURE 368:32-38(1994).
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PLASMID PMT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAX).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
ELASMOBRANCHII; RAJIFORMES; TORPEDINOIDEI; TORPEDINIDAE; TORPEDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 92064638.
TEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
"Dystrophin is a component of the subsynaptic membrane.";
J. CELL BIOL. 115:1069-1076(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70; DB 5; Length 426;
Pred. No. 1.23e+00;
4; Mismatches 7; Indels
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                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
GATTUNG S. GOELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
WATERSTON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                             EMBL; AF003739; G2105488; -...
PROSITE; PS00627; GHWP_KINSES_ATP; 1.
PROSURE GHMP_KINSESS. 1.
SEQUENCE 426 AA; 47290 MW; 7CBEF743 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           883 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 ECSCRELDEICRLY-LDHGALGARLTG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | : : | | | | | | | | | 5 DC-CRQKTCSCRLYELLHGA-GNHAAG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane of Torpedo electric organ. J. PHYSIOL. (PARIS) 0:131-133(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PROSITE; PS01159; WW_DOMAIN_1; 1.
PRAM; PP000397; WW_rsp5_WWP; 1.
PFAM; PF00435; spectrin; 2.
PFAM; PF00569; 22; 1.
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Local Similarity 61.5%;
Les 8; Conservative
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07,
07,
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Best Local Similarity 48.1%;
Matches 13; Conservative
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ID 068770 PRELIMINARY;

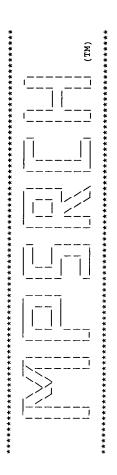
AC 068770,

DT 01-AUG-1998 (TREMBLREL. 07

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DT 01-AUG-1998 (TREMBLREL. 07
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
DYSTROPHIN (FRAGMENT).
                      NATURE 368:32-38(1994).
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| 19 LLHGAGNHAAGIL 31
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elegans.";
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091493;
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BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA
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MAIDEN M.C.J., BYGRAVES J.A., FEIL E., MORELLI G., RUSSELL J.E.,
URWIN R., ZHANG Q., ZHOU J., ZURTH K., CAUGANT D.A., FEAVERS I.M.,
ACHTMAN M., SPRATT B.G.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF037797; G2745813; -.
                                                 BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
YERSINIA.
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                                                                                                                                                                                                                                                      Query Match 27.3%; Score 70; DB 2; Length 1135; Best Local Similarity 47.4%; Pred. No. 1.23e+00; Matches 9; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 163;
                                                                                                                                          , GARNES J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-KIM;
HU P., ELLIOTT J., MCCREADY P., SKOWRONSKI E., GARNES
KOBAYASHI A., CARRANO A.V., BRUBAKER R., GARCIA E.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
PLASMID.
                                                                                                                                                                                                                        SEQUENCE 1135 AA; 126286 MW; 4EED77D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB 2; L4
Pred. No. 1.82e+00;
7; Mismatches 9
ONA POLYMERASE III ALPHA SUBUNIT HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: Fri Aug 20 21:08:05 1999 Job time : 41 secs.
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                                                                                                                                                                                                                                                                                                                               474 ACKLQSLMRGFGRHAAGMI 492
                                                                                                                                                                                                                                                                                                                                                      13 SCRLYELLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%;
Similarity 34.6%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                     [1]
SEQUENCE FROM N.A.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

MasPar time 4.51 Seconds 132.123 Million cell updates/sec Run on:

Fri Aug 20 21:09:47 1999;

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201

Description: Perfect Score:

PAM 150 Gap 15 Scoring table:

Sequence:

1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseq35 Database:

scale 0.251 Variance 88.282; Mean 22.192; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

NO.	11	11	11	11	10	01	0.1	01	02	02	02	02	02	02	02	02
Pred. 1	2.26e-1	2.26e-1	2.26e-1	2.26e-1	2.79e-1	6.37e+0	6.37e+0	9.27e+0]	1.12e+0	1.12e+02	1.12e+02	1.34e+0	1.34e+02	1.34e+02	1.34e+02	1.34e+02
Description	Mouse HFGAN72 recepto	Rat HFGAN72 receptor	Mouse hypocretin 35.	Rat hypocretin 35.	Human HFGAN72 recepto	LexA/NuMA fusion prot	GAL4/HA/NuMA fusion p	"p33" N-terminal (2).	Retinoid X receptor i	Human recombinant col	Protein (OA-519) cros	Deduced sequence of h	MY17 preproPR-3.	KM31-7 precursor.	Human KM-102-derived	S. cerevisiae scaur2R
ID	W61383	W61382	W50158	W50157	W61381	W21732	W21731	R20235	R99737	W68485	W32881	R45403	R85639	R92050	W83404	R67691
DB	33	33	30	30	33	23	23	4	18	35	24	σ	12	16	38	13
% Query Match Length DB	123	130	130	130	131	2192	2272	10	716	1464	2509	256	256	549	551	1477
% Query Match	100.0	100.0	100.0	100.0	94.5	33.8	33.8	32.8	32.3	32.3	32.3	31.8	31.8	31.8	31.8	31.8
Score	201	201	201	201	190	89	68	99	65	65	65	64	64	64	64	64
Result No.	1	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16

Saccharomyces cerevis 1.34e+02 Ecdysone receptor 11.62e+02 Drosophila ecdysone re 1.62e+02 Modified ecdysone rec 1.62e+02 Modified ecdysone rec 1.62e+02 Ecdysone receptor 1.62e+02 DRR3alpha protein. 1.62e+02 DRR3alpha protein. 1.62e+02 Tylactone synthase OR 1.62e+02 Tylactone synthase OR 1.62e+02 Tylactone synthase OR 1.62e+02 Human alpha-1 collage 1.94e+02 Human alpha-1 collage 1.94e+02 Human alveolar surfac 2.33e+02 Plasmid pASPC-SV(10) 2.33e+02 Sequence deduced from 2.33e+02 Sequence deduced from 2.33e+02 Genomic sequence of human alv ASP encoded 2.33e+02 Human 32K ASP encoded 2.33e+02 Human 32K ASP encoded 2.33e+02 Human 32K Alveolar su 2.33e+02 Human 32K Alveolar su 2.33e+02 Human marcoSR protein 2.33e+02	NTS  renal disease; heart failure; arkinson's disease; urinary retention; cardial infarction; psychotic disorder; s	Wilson S, Yanagisawa M;  prresponding DNA, agonists,  ains two ligans whose antagonists can be es, anorexia nervosa, bulimia, cachexia, ease, congestive heart failure, impaired unction. The agonist is useful for and cachexia. The HEGAN72 receptor i. bacterial, fungal, protozoan and viral ns caused by HIV-1 or HIV-2, pain, a, cachexia, obesity, diabetes, asthma, and congestive heart failure, iy retention, osteoporosis, angina ulcers, asthma, allergies, benign
WW105424 WW395133 WW395133 WW336555 WW336554 WW20605 W	ALIGNMENT 123 AA. tein. itsorders; insorders; ris; myoca ris; myoca qand 728"	17-DEC-1995; 310216. 26-SEP-1997; 310216. 26-SEP-1997; US-939093. 17-DEC-1996; US-93504. 19-MAR-1997; US-820519. 02-JUL-1997; US-887382. (SMIK ) SMITHKLINE BEECHAM FOC. BETGRAM DJ, BROOKS DP, Gellai M, Wilson WPI; 98-324672/29. HFGAN/2 receptor ligands - and corresponding in the HFGAN/2 receptor protein contains the HFGAN/2 receptor protein contains to used for treating obesity, diabetes, and chronic renal failure, renal disease, of chronic renal failure, renal disease, directions concerns anorexia nervosa, bulimia and ligand is useful for treating e.g. bact infections, particularly infections cancers, anorexia nervosa, bulimia, carpanets, anorexia nervosa, bulimia, carpatkinson's disease, both acute and con hypotension, hypertension, urinary reterpectoris, myocardial infarction, ulcers
20222 202220	in; 12 try) try) prote ng dis V; can ectori con/Qua "Liga	HAM HAM Gel ss - eat ty, rey, rey, y i sa, th, oon,
1477 1467 1477 1467 1467 1467 167 167 167 167 167 167 167 167 167 1	rd; Protein; (first entry) receptor pro tor; eating d tor; eating angina pecto disorder. Location/Q 33.65 /note="Li 69.98	216. 939993. 939093. 8203104. 887382. 887382. 887382. 911gan BEEC. 911gan BEEC. 920. 935pp; E 35pp; E 35pp; E 31pp. 94 obesit liure. 95 a nervo an ervo an erv
	tandard; 998 (fi 9AN72 re receptor ysfuncti osis; an ical dis	997; 310216. 997; US-93999 997; US-93999 997; US-93999 997; US-887382 SMITHKLINE BEE EXMITHKLINE BEE EXMITHKLINE BEE SMITHKLINE BEE AND FROM SMITHKLINE AND
4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	W61383 standa W61383 standa W61383; W61384; W6026-1998 Mouse HFGAN72 HFGAN72 recep Sexual dysfun osteoporosis, neurological Mus sp. Region Region	- UEC-197 - SEP-197 - UEC-197 - UIL-198 - UIL-
11112222222222222222222222222222222222		PR 17. PR 19. PR

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JT 6
W21732 s
W21732;
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BY THY CAN'S TENCEPTOR 11990.

Claim 2: Fig 2: 35pp; English.

Claim 3: Fig 2: 35pp; English.

Claim 4: Fig 2: 35pp; English.

Claim 5: Fig 2: 35pp; English.

Claim 6: Fig 2: 35pp; English.

Claim 7: Fig 2: 35pp; English.

Claim 6: Fig 2: 35pp; English.

Claim 7: Fig 2: 35pp; English.

Claim 6: Fig 2: 35pp; English.

Claim 7: Fig 2: 35pp; English.

Claim 6: Fig 2: 35pp; English.

Claim 7: Fig 3: 5pp; English.

Claim 6: Fig 3: 5pp; English.

Claim 7: Fig 3: 5pp; English.

Claim 6: Fig 3: 5pp; English.

Cla
                                                                                                                                                                                                                                                                                                                                                                                                          Human HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure;
Execual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder.
                                                                                                                                                                                                      ö
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonuclectides based on H35 cDNA can be used to detect the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor.
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 190, DB 33; Length 131;
Pred. No. 2.79e-10;
2; Mismatches 0; Indels
                                                                                                                                                             Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFGAN72 receptor ligands - and corresponding DNA, agonists
                                                                                                                                         Score 201; DB 30; Length Low
Pred. No. 2.26e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Bergsman DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI; 98-334672/29.
N-PSDB; V28138.
                                                                                                                                                                                                                                        69 rpgppglqgrlqrllqangnhaagiltm 96
                                                                                                                                                                                                                                                                              1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34..66
/note= "Ligand 72A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Ligand 72B'
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W61381 standard; Protein; 131
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Best Local Similarity 92.9%;
Matches 26; Conservative
                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-1997; US-939093.
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19-MAR-1997; US-820519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1997; 310216
                                                                                                                       130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                             W61381;
02-OCT-1998
                                                                                                                         Sequence
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Indiguous, the sequences given in W21731-32 represent fusion proteins which contain. The sequences given in W21731-32 represent fusion proteins which contain. NuMA (nuclear mitoric apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
                                                                 LexA/NuMA fusion protein.
The I, NIP-1, NIP-2, NUMA; nuclear mitotic apparatus; NuMA interacting protein;
cell division; proliferation; antibody; Ab; detection;
malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding nuclear mitotic appts. interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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365..1864
/label= Coiled_coil_region
                                                                                                                                                                                                                                                                                              /label- Residues_18-2116_of_NuMA
285..1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 23; I
Pred. No. 6.37e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= GAL4_DNA_binding_domain
                                                                                                                                                                                                                             /label= LexA_DNA_binding_domain
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/label= Hemaglutinin_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                               /label- Coiled_coil_region
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                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                    88..94
/label- Polylinker
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standard; Protein; 2192 AA
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Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: | ||::|||:||:||:||1 RPGPPGLQGRLQRLLQAN 18
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01-OCT-1997 (first entry)
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Snyder MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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07-JUN-1995, US-478408.
(UYYA.) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McPherson SMG, Sny
WPI; 97-077270/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T77783
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Best Local S
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Disclosure; Fig 7; 138pp; French.

The invention relates to the production of mammalian collagen type I gene carbon alpha22, spanning the human collagen type I gene were isolated from a MG-63 osteosarcoma library. Clone alpha3 contained 83 bp of the 5 untranslated region and the first 1920 bp of coding 83 bp of the 5 untranslated region and the first 1920 bp of coding 171-1454 of the protein and around 500 bp of the 3' untranslated region. The 2 clones were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The fragments are: (B) containing nucleotides (nt) -4 to 479;

CC (pathogenesis related protein S) signal peptide and bases 66-77 from the sequence encoding the N-terminus of the pro-collagen amino propeptide domain; (C) the whole of the amino propeptide domain (nt 72-479); (D) all of the whole of the amino propeptide domain (nt 535-1920); (E) the DraIII-BamHI fragment (1709-2808) of alpha22, encoding as 567-936 of the central helicoidal domain; (F) the BamHI-ECARI (2803-4562) region of alpha22, encoding as 396-1192 in the central helicoidal domain and as 1193-144 in the C-propeptide domain; (G) the C-terminus of the C-propeptide domain; (G) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as prostheses for cardiac valves, ligaments or tendons; skin substitutes; gingival implants; microcapsules for perfumes; guide tubes for nerve regeneration; slow release products for antibiotics, growth factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anticancer agents or anti-inflammatories; surgical thread and components of ointments). They are suitable for treating any disorder related to collagen dysfunction and gelatin, produced from collagen, is used to produce glues, surgical prostheses and foods.

Sequence 1464 AA:
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Protein (OA-519) cross-reactive with hpr gene product.
OA-519; cross-reaction; haptoglobin related; hpr; antibody; epitope; haptoglobin 1; haptoglobin 2; cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 35; Length 1464; Pred. No. 1.12e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W32881 standard; Protein; 2509 AA W32881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%;
imilarity 64.3%;
9; Conservative
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Kuhajda FP, Pasternack GR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 JAN-1989; US-297722.
04 -DEC-1990; US-622407.
26 -UUL-1991; US-315522.
24 -JUL-1992; US-917716.
26 -JUL-1993; US-096908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 pgppglggklapgl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PGPPGLQGRLQRLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-188426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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PR-3; preproPR-3; MY17; human neutrophil protease-3; serine protease; tumour necrosis factor alpha; Thealpha; HL60; MY17; B cell; T cell; tumour necrosis factor alpha convertase; cytokine; septic shock; rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease; ischaemia/reperfusion injury; autoimmune disease; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and treating sepsis, AIDS, auto-immune disease etc.
Disclosure; Fig 2; 69pp; English.

ProTNE refers to TNE having a molecular weight of about 26,000,
which is the prohormone form of TNFa. ProTNE is cleaved to a lower
molecular weight mature' form, pref. 17kb, which, in its multimeric
(usually trimeric) form, is substantially involved in producing life-
threatening physiological changes associated with sepsis. ProTNF is
cleaved by convertase. One TNF convertase is serine protease
proteinase-3, also called PR-3, P-29B or myeloblasin. A suitable
source of convertase is the HL60 cell line (or extracts, or the
culture media in which it is grown). The convertase produced by
HL60 has been sequenced and is identical to the known lymphocyte
serine protease PR-3 which has other activities unrelated to TNF
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cpds. which inhibit formation of mature tumour necrosis factor from its precursor - identified using TNF convertase, e.g. mutein(s), antibodies or peptide phosphonate(s), for preventing and treating sepsis, AIDS, auto-immune disease etc.
Claim 2; Columns 43-60; 68pp; English.#
The present sequence is a protein (OA-519) cross-reactive with the haptoglobin related (hpr) gene product. OA-519 can be used raise antibodies reactive with epitopes found on the hpr gene product, but not on haptoglobin 1 or 2, useful in cancer, especially breast cancer, prognosis assays.
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                                                                                                                                                                                                                                                                      Length 2509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deduced sequence of human proteinase-3 (PR-3)
TNF convertase; proteinase-3; PR-3; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CETU ) CETUS ONCOLOGY CORP.
Halenbeck RF, Jewell DA, Koths KE, Kriegler M, Perez C;
                                                                                                                                                                                                                                           Score 65; DB 24; Lengtn 200
Pred. No. 1.12e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.8%; Score 64; DB 9; Length 256; Best Local Similarity 38.5%; Pred. No. 1.34e+02; Matches 10; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               411 ppapaphatlprllrasgrtpeavgkl 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PGPPGLQGRLQRLLQANGNHAAGILTM 28
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R45403 standard; Protein; 256 AA.
R45403;
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R85639 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                          32.3%;
29.6%;
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                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1993; U06120.
25-JUN-1992; US-905546.
                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                         2509 AA;
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Location/Qualifiers

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Fri Aug 20 21:12:58 1999; MasPar time 1.89 Seconds 150.169 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

106580 segs, 10152877 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Mean 20.582; Variance 81.576; scale 0.252 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Pred. No.	•	2.72e+01	2.72e+01	2.72e+01	2.72e+01	3.30e+01	4.00e+01	4.00e+01	5.87e+01	7.10e+01	8.57e+01	8.57e+01	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02						
Description		Sequence 4, Applicatio	11,	S,	12,	'n	4	10,	ý	2,	'n	Sequence 1, Applicatio	'n	4	7	ὼ	4,	4,	Sequence 2, Applicatio	14,	4, A	14,	Sequence 4, Applicatio	4,
ID		us-08-363-	us-08-363-	US-08-363-	US-08-363-	PCT-US91-0	PCT-US95-1	US-08-469-	US-08-804-	US-08-494-	US-08-858-	US-08-858-	PCT-US93-0	US-07-949-	US-08-115-	US-08-792-	US-08-814-	US-08-017-	US-07-941-	US-07-921-	PCT-US93-0	PCT-US94-1	08-11	US-07-941-
· 80	1	7	~	7	7	m	m	Н	7	Н	7	7	m	-	Н	Н	7	~4	Н	Н	r	m	Н	Н
Length		442		445	445	10	716	50	1841	69	381	381	199	199	199	199	199	199	199	296	296	296	296	. 296
% Query Match		33.3	33.3	33.3	33.3	32.8	32.3	ď	31.3	30.8	Ö	•	ص	29.9	ő.	29.9	o,	29.9	o,	σ.		29.9	29.9	29.9
Score		67	67	67	. 67	99	65	65	63	62	61	61	09	09	09	9	9	9	09	9	09	09	09	9
Result No.	1 1 1	-	7	3	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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Sequence 4, Application PC/TUS9516311
GENERAL INFORMATION:
APPLICANT: MOOF, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hueng-Sik
TITLE OF INVENTION: PETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 3; Length 10;
Pred. No. 3.30e+01;
1; Mismatches 0; Indels
                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311 FILING DATE:
                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US91/04588
FILING DATE: 19910627
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/544,862
FILING DATE: 27-JUN-1190
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                         COUNTRY: USA
ZIP: 10022-6250
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9516311
                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-715-0600
TELEX: 112-715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
ENCE 10 AA; 1169 MW; 376 CN;
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%;
88.9%;
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STATE: MA
COUNTRY: USA
TO: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                          New York
    New York
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Best Local Similarity
Matches 8; Conserv
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ID PCT-US95-16311-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GLEGRLQRL 9
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                                                                                                                                          APPLICANT: COLLINS, DESMOND M.
APPLICANT: GOLLINS, DESMOND M.
APPLICANT: de LISLE, GEOFFREY W.
APPLICANT: PASCOPELLA, LISA
APPLICANT: RANARAMI, RIKU P.
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%; Score 67; DB 2; Length 445; 31.8%; Pred. No. 2.72e+01; Ative 11; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                      STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
2 IP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application PC/TUS9104588
GENERAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Ware, Carl F.
TITLE OF INVENTION: SURFACE COMPLEXED LYMPHOTOXIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O Fish & Neave
STREET: 875 Third Avenue, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION UNMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20002.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAS: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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445 AA; 48583 MW; 967304 CN;
                                                                                                       JACOBS, Jr., WILLIAM R. BLOOM, BARRY R.
                                     Sequence 12, Application US/08363255
Patent No. 5783386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS9104588
Sequence 12, Application US/08363255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 LQEQLHSVLDTLSEREAGVVSM 394
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| LQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity 31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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COUNTRY:
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                      Gaps
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Patent No. 5731192
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Length 1841;
                      8; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                            1694 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AA.
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Pred. No. 7.10e+01;
Query Match 31.3%; Score 63; DB 2; L
Best Local Similarity 33.3%; Pred. No. 5.87e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40397/104/BABR
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE TYPE: protein
1694 AA; 165283 MW; 14956750 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BEINHAID D.
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                            Sequence 2, Application US/08494168
                                         1513 RDTPAALAAHLAELLATARDHGPG 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                        1694 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                       Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                      8; Conservative
                                                                                                                                                                                                                                                                                                               CITY: WALL
COUNTRY: USA
TO: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1028 RPGPPGLPG 1036
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US-08-494-168-2
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                      Matches
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Sequence 3, Application US/08858052
Patent No. 5849498
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN 3-HYDROXXISOBUTYRUL-COENZYME A
TITLE OF INVENTION: HUMAN 3-HYDROXXISOBUTYRUL-COENZYME A
TITLE OF INVENTION: HYDROLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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Pred. No. 8.57e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,052
FILING DATE: Herewith
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1575573
UENCE 381 AA; 42837 MW; 742169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.3%;
Best Local Similarity 26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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Length 199;

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Patent No. 5437863
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
                                                                                                                                                   Score 60; DB 1; Length 199;
Pred. No. 1.03e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                        199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/941,372
FILING DATE: 02-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
                   NAME: Meinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: 5174BPCT
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE IYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08115680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 199 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19477
COMPUTER READABLE FORM:
                                                                                                                                                   29.9%;
Similarity 70.0%;
7; Conservative
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                                                                                                                                                               Best Local Similarity
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US-08-115-680-2
                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGBMT INFORMATION:
NAME: COOK, ROBERT R.
REFERENCE/DOCKET NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 31,602
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          Sequence 8, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
Score 60; DB 1; Leng
Pred. No. 1.03e+02;
                                                                                                                     199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 1; L
Pred. No. 1.03e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                               STREET: 1840 DEHAVILLAND DRIVE CITY: THOUSAND OAKS STATE: CA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IION: -21..0
199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: Fri Aug 20 21:13:06 1999 Job time: 8 secs.
                                                                                                                                                                                       Sequence 8, Application US/08792019B
                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
     Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
LOCATION: 1..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                   129 LQARLDRLLR 138
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                                                               ||:||:||:
| LQGRLQRLLQ 16
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7 LQGRLQRLLQ 16
                                                                                                                    US-08-792-019B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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Fri Aug 20 21:11:47 1999; MasPar time 6.52 Seconds 234.409 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_nammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 30.180; Variance 51.706; scale 0.584 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

4							
No.	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.
-	201	100.0	130	11	055241	HYPOCRETIN (PREPRO-ORE	4.74e-26
7	201	100.0	130	11	055232	PREPRO-OREXIN.	4.74e-26
m	197	98.0	131	9	077668	PREPRO-OREXIN PRECURSO	3.52e-25
4	190	94.5	131	4	043612	PREPRO-OREXIN.	1.15e-23
Ŋ	16	37.8	1174	9	095168	TIGHT JUNCTION PROTEIN	2.98e-01
9	75	37.3	1277	11	035821	PAR INTERACTING PROTEI	4.31e-01
7	73	36.3	249	11	P97382	K+ CHANNEL BETA4 SUBUN	8.98e-01
ω	71	35.3	145	10	048721	T9J22.21 PROTEIN.	1.85e+00
σ	70	34.8	511	10	080740	T13D8.6 PROTEIN.	2.64e+00
10	69	34.3	331	13	091640	LEUCINE ZIPPER WITH BA	3.76e+00
11	69	34.3	389	11	088539	WW DOMAIN BINDING PROT	3.76e+00
12	99	33.8	162	~	082680	RNA POLYMERASE SIGMA-L	5.34e+00
13	68	33.8	481	m	042651	HYPOTHETICAL 55.5 KD P	5.34e+00
1,4	9	33.8	1015	10	064673	F22013.25.	5.34e+00
15	99	33.8	2115	4	014980	NUMA PROTEIN.	5.34e+00
16	67	33.3	161	7	085683	RNA POLYMERASE SIGMA-L	7.55e+00
17	67	33.3	178	7	031955	YONC PROTEIN.	7.55e+00
18	67	33.3	178	σ	064066	HYPOTHETICAL 19.6 KD P	7.55e+00
19	67	33.3	413	11	035141	MAXP1.	7.55e+00
20	67	33.3	462	7	P95644	RNA POLYMERASE SIGMA F	7.55e+00

7.55e+00 7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01
RNA POLYMERASE SIGMA F MAJOR VEGETATIVE SIGMA	RNA POLYMERASE SIGMA F	RNA POLYMERASE SIGMA F	RNA POLYMERASE SIGMA F	HYPOTHETICAL 60.1 KD P	ARTICULIN P60.	DNA POLYMERASE III TAU	HRPG.	DEOXYCYTIDINE-TRIPHOSP	UNKNOWN GENE.	D-SUBUNIT OF BENZOYL-C	T24D5.1 PROTEIN.	RNA-DIRECTED DNA POLYM	THYROID HORMONE INDUCE	HYPOTHETICAL 41.3 KD P	CARA.	H06001.2 PROTEIN.	PRISTINAMYCIN I SYNTHA	TNA2, TNA1, PARTIAL AN	TRANSCRIPTIONAL ACTIVA	RETINOID X RECEPTOR IN	P160 MYB-BINDING PROTE	PUTATIVE ABC TRANSPORT	FATTY ACID SYNTHASE (E
Q59913 O50539	P77951	059813	059814	069851	027212	045998	060245	027642	054224	087877	922732	005804	091654	969600	050983	017909	054959	050648	050205	060811	035851	081016	016702
77	7	7	7	7	S	7	7	-	7	~	S	7	13	ນ	7	Ŋ	~	7	7	11	11	10	4
510 511	514	525	528	541	268	809	130	150	253	282	304	319	335	365	377	1465	2591	213	443	580	1344	1420	2509
33.3		33.3	33.3	33.3	33.3	33.3	32.8	32.8	32.8	•	32.8	32.8	32.8	•			32.8	32.3	32.3	32.3	32.3	32.3	32.3
67	67	29	29	67	67	67	99	99	99	99	99	99	99	99	99	99	99	65	65	65	65	9	65
21	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                          36.3%;
ilarity 76.9%;
Conservative
                                                                                                                                                                                                                                                                                       90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                      01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                    21 PHPPGLQGSLDRL 33
                                                                                                                                                                                                                        14
                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                1 |||||| |:||
2 PGPPGLQGRLQRL
                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                     T9J22.21 PROTEIN.
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                                           TISSUE-BRAIN
                                                                                                                                                                                  10;
                                                                                                                                      SEQUENCE
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O80740;
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048721
048721;
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EURARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                             SEQUENCE FROM N.A.
MEDLINE: 96421547.
BEATCH M., JESATIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.;
"The tight junction protein ZO-2 contains three PDZ
(PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91084854.

WUARIN J., SCHIBLER U.;

"Expression of the liver-enriched transcriptional activator protein
DBP follows a stringent circadian rhythm.";

CELL 63:1257-1266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75; DB 11; Length 1277;
Pred. No. 4.31e-01;
14; Mismatches 5; Indels
                                                                                                                                                                                                                                            Length 1174;
                                                                                                                                                                                                                                          Score 76; DB 6; Length 1174
Pred. No. 2.98e-01;
12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. COMIE P.A., OSSIPOW V., SCHIBLER U.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                           GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                 BEATCH M.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (2015): G155970; -.
FRAM; PRO0595; PDZ; 3.
PFAM; PF006295; Guanylate kin; 1.
PFAM; PF006295; Guanylate kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE) ·
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1277 AA; 144674 MW; 89721F79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AA.
                                                                                                                                                                                                                                                                                                                                                  PRT; 1277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                   268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295
                                                                                                                                                                                                                                                                                                 BIOL. CHEM. 271:25723-25726(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826 PGAEALHAQVERFVQQAGNQADASVAL 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||::|::|::|
PGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
Or suppressor protein.";
CELL BIOL. 124:949-961(1994).
                                                                                                                                                                                                                                                                                                                                                                       05,
08,
                                                                                                                                                                                                                                         Query Match 37.8%;
Best Local Similarity 32.1%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TREMBLREL. 03, 01-MAY-1997 (TREMBLREL. 03, 01-NOV-1998 (TREMBLRELL. 08, K+ CHANNEL BETA4 SUBUNIT. MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.3%;
Local Similarity 29.6%;
Les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
PAR INTERACTING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U83590; G2253211;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                    region.";
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P97382;
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  tumor
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPRALES; BRASSICACEAE; ARABIDOPSIS.
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERNATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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STRAIN=CV. COLUMBIA;
STRAIN=CV. SCHWARIZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
VYSOTSKAIA V.S., SCHWARIZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
LIU S., LI J., ARALON R., AU M., BRENDEL V., BUEHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURIZ D., LI Y., PALM C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                 LAZDUNSKI M.; "A new K+ channel beta subunit to specifically enhance Kv2.2 (CDRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                          BARHANIN J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
STONINSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC002505; G2739379; --.
SEQUENCE 145 AA; 15355 MW; 660DDF14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 11; Length 245
Pred. No. 8.98e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.3%; Score 71; DB 10; Length 145 Best Local Similarity 39.1%; Pred. No. 1.85e+00; Matches 9; Conservative 8; Mismatches 6; Indels
                                                                                                                                                    MEDLINE; 96421640.
FINK M., DUPRAT F., LESAGE F., HEURTEAUX C., ROMEY G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                        249 AA; 27749 MW; 8805DBE7 CRC32;
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                                                                                                                                                                                                                                                                                 expression.";
J. BrOL. CHEM. 271:26341-26348(1996).
EEMBL; U65593, G1695272; -.
IONIC CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
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1 RPGPPGLQGRLQRLLQAN 18

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Search completed: Fri Aug 20 21:12:40 1999 Job time : 53 secs.
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RA MAEKAWA T., KURIYAMA R.;

RA MAEKAWA T., KURIYAMA R.;

RT "Primary structure and microtubule-interacting domain of the SP-H

RT antigen: a mitotic MAP located at the spindle pole and characterized

RT antigen: a mitotic MAP located at the spindle pole and characterized

RT as a homologous protein to NuMA.";

J. CELL SCI. 105.589-600(1993).

BMBL; 211583; G35119;

CONFLICT 124 124 0 -> P (IN REF. 2).

TONFLICT 1587 1587 0 -> H (IN REF. 2).

TONFLICT 1587 1587 0 -> H (IN REF. 2).
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUMA PROTEIN.
HOMO SAPIENS (HUMAN).
EDKARYOTA: METAZOA: CHORDATA: VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                01-40G-1998 (TREMBLREL. 07, CREATED)
01-40G-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-40G-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-40G-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
F22013.25.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE, STRETOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA, MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURICE FROM N.A.
MEDLINE, 92176231.
YANG C.H., LAMBIE E.J., SNYDER M.;
"NuMA: an unusually long colled-coll related protein in the mammalian nucleus.";
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SHINN P., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN H.,
CONWAY A., CONNAY A., KURTZ D., OJI O., SHEN Y.K., TORIDMI M.,
VYSOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.8%; Score 68; DB 10; Length 1015; Best Local Similarity 50.0%; Pred. No. 5.34e+00; Matches 13; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 4; Length 2115;
Pred. No. 5.34e+00;
6; Mismatches 3; Indels
   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC003981; G3063463; -.
SEQUENCE 1015 AA; 111751 MW; 82FA3G3F CRC32;
 Mismatches
                                                                                                                                      PRT; 1015 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 2115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 PTRPGLRSSLKRKRGNNGPTAATILT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PGPPGLQGRLQRLLQANGNHAAGILT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL BIOL. 116:1303-1317(1992).
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761 RAGRKGLEARLQQLGEAH 778
                                 280 LQEVLQSDSNHVPSVLT 296
 Conservative
                                                     || :||:::|| :::||
|11 LQRLLQANGNHAAGILT 27
                                                                                                                                    PRELIMINARY;
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                                                                                                                                                    064673;
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Q14980
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064673
 Matches
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:11:16 1999; MasPar time 3.39 Seconds 233.546 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Description: Perfect Score:

PAM 150 Gap 15 Scoring table:

Sequence:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.574; Variance 48.443; scale 0.652

# SUMMARIES

Pred. No.	9	DISMUTASE { 6.21e-01	i	96.8 KD P 1.	2.82e+00	E PRINCIP 2.82e+00	BIOSYNTHESI 2.82e+00	PROTEIN E2. 4.07e+00	MGEN 36. 5.86e+00	VP1. 5.86e+00	ιυ ·	LASE (EC 5.86e+00	.1 PRECURS 8.40e+00	PRECURSOR 8.40e+00	TASE (FER 8.40e+00	SISTANCE 8.40e+00	28 KD PRO 1.20e+01	40S RIBO 1.	PEPTIDE 1.20e+01	63.2 KD P 1.20e+01	'ATE ADENY 1.20e+01	10.100 1 4 44 0 05
Description	SUPEROXIDE DI	SUPEROXIDE DISMUTASE (	ADRENOLEUKODYSTROPHY	HYPOTHETICAL	NIFU PROTEIN.	RNA POLYMERASE	PEROXISOME BI	REGULATORY PR	CUTICLE COLLAGEN	COAT PROTEIN VP1.	SERINE/THREONINE PROTE	ADENYLATE CYCLASE	INTERLEUKIN-11 PRECURS	MYELOBLASTIN PRECURSOR	SULFITE REDUCTASE	OLIGOMYCIN RESISTANCE	HYPOTHETICAL 28	MITOCHONDRIAL	MITOCHONDRIAL	HYPOTHETICAL	PROBABLE SULFATE	1 1 0 1 20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ID	SODC_HAEPA	TR12 HIMAN	ALD_MOUSE	YDBH_ECOLI	NIFU_FRAAL	HRDB_STRCO	PEX1_PICPA	VE2_HPV63	CC36_CAEEL	COA1_POVLY	AFSK_STRCO	CYAA_SCHPO	IL11_MOUSE	PRN3_HUMAN	SIR_SYNP7	YOR1_YEAST	YPE1_RHORU	RT04_YEAST	RF1M_HUMAN	YEAJ_ECOLI	NODQ_RHISB	F 1000
DB		٦.	٦,	Н	Н	Н	Н	Н	Н	Н	Н	Н	~	-	Н	-	Н	~	Н.	_	-1	-
% Query Match Length	000	1992	m	879	79	442	1157	398	307	368	799	1692	199	256	624	1477	255	394	445	556	633	70,0
% Query Match	35.3	34.3		٠	33.3	æ.			32.3		32.3	32.3	31.8	31.8	31.8	31.8	31.3	31.3	31.3	31.3	31.3	, ,
Score	17,	69	99	99	67	49	49	99	65	65	65	65	64	64	64	64	63	63	63	63	63	63
Result No.	, c	7 M	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.20e+01 1.20e+01	1.70e+01	1.70e+01	1.70e+01 1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01	2.41e+01
ECDYSONE RECEPTOR (ECD HYPOTHETICAL PROTEIN K	HIPOTHETICAL 28: / KD P FACTOR VIII INTRON 22	Æ,	RNA POLYMERASE SIGMA F COLLAGEN ALPHA 1(XVIII	COLLAGEN ALPHA 6(IV) C	COLLAGEN ALPHA 4(IV) C	COLLAGEN ALPHA 2(IV) C	PROCOLLAGEN ALPHA 2(IV	HYPOTHETICAL PROTEIN M	NEGATIVE FACTOR (F-PRO	TRANSCRIPTIONAL REGULA	HYPOTHETICAL OXIDOREDU	PULMONARY SURFACTANT-A	RETINA SPECIFIC REGULA	BETA-ARRESTIN 2.	ADENOSYLHOMOCYSTEINASE	LEGUMIN B PRECURSOR (B	PHEROMONE B ALPHA 2 RE	PROBABLE DNA PACKAGING
ECR_DROME Y310_HUMAN	F812_MOUSE	ASSY_SYNY3	RPSD_CAUCR CA1H_HUMAN	CA64_HUMAN	CA44_HUMAN	CA24_CAEEL	CA24_ASCSU	Y652_METJA	NEF_HV2NZ	BASR_SALTY	YDGB_ECOLI	PSPA_HUMAN	RGSX_BOVIN	ARR2_HUMAN	SAHH_PYRHO	LEGB_GOSHI	BAR2_SCHCO	VTER_EBV
		Η,		П	Н	Н	Н	П	Н	٦	П	7	_	г	Н	7	-	-
878 881	380	400	652 684	1678	1690	1758	1763	134	180	222	240	248	374	409	421	516	518	069
31.3	30.8	30.8	30.8	30.8	30.8	30.8	30.8	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3
63	6 6 6 6	62	2 6	62	62	62	62	61	61	61	61	61	61	61	61	61	61	61
25	27	28	3.0	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORLUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMORA S., KITAGAWA M., KITAKAWA M., MAKINO K., MASUDA S., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                    SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE: 9742647.
BLATTHER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
                                                                                                        GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTINOMYCETALES; FRANKINEAE; FRANKIACEAE; FRANKIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 1; Len
Pred. No. 1.94e+00;
6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I -> L (IN REF. 3).
8BFD7CF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95369734.
HARRIOTT O.T., HOSTED T.J., BENSON D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RUDD K.E.;
UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000235; G1787646; -.
EMBL; D90776; G1742260; -.
EMBL; D90777; G1742264; -.
EMBL; U36928; -; NOT_ANNOTATED_CDS.
ECCOGENE; EG13180; YDBH.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GLQGRLQRLLQANGNHAAG-ILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               879 AA; 96834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,
32,
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                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION
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  ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANKIA ALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12;
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROBABLE).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adrenoleukodystrophy gene.";
MAMM. GENOME 5:810-813(1994).
-!- FUNCTION: PROBABLE TRANSPORTER. COULD BE INVOLVED IN THE
IMPORT OF VLCFA-COA SYNTHETASE INTO THE PEROXISOMAL MEMBRANE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:99672; ALDGH.
PROSTIE: PSOOGII, ABC_TRANSPORTER; 1.
PFAM; PFOONO5; ABC_TRAN; 1.
ATP-BINDING; GLYCOPROTEIN; TRANSMEMBRANE; TRANSPORT; PEROXISOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                     SARDE C.O., THOMAS J., SADOULET H., GARNIER J.M., MANDEL J.L., "CDNA sequence of Aldgh, the mouse homolog of the X-linked
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P52645; P77502; P76855; (1-00T-1996 (REL. 34, CREATED) (1-00T-1996 (REL. 34, LAST SEQUENCE UPDATE) (REL. 35, LAST SEQUENCE UPDATE) (REL. 35, LAST SEQUENCE UPDATE) HYPOTHETICAL 96.8 KD PROTEIN IN LDHA-TYNA INTERGENIC REGION.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P (BY SIMILARITY).
D373B00E CRC32;
7
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                                                                                                                                                                                           01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEDUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADRENOLEUKODYSTROPHY PROTEIN HOMOLOG (ALDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
4; Mismatches
                                                                                                                                                         736 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 704 AGIPKMOGRLQELRQILGEAAAPVQPL 730
                                                                                                                                                                                                                                                                                                                                                                                                                               SARDE C.O., THOMAS J., SADOULET H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| | :||||| | | |: || : : | PGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 44.4%;
Matches 12; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z33637; G520955; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                         STANDARD;
                                                                                                                                                                   P48410;
01-FEB-1996 (REL. 33, CF
01-FEB-1996 (REL. 33, L)
01-FCB-1997 (REL. 35, L)
                                    289 KPGPSGLQAKLASL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258
353
493
                                                          :|||:|||:|| | 1
1 RPGPPGLQGRLQRL 14
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=FIBROTIC LIVER;
MEDLINE; 95201443.
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473
507
736 AA;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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       noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAWLITA M., CLAD A., ZUR HAUSEN H.;
"Complete DNA sequence of lymphotropic papovavirus: prototype of a mew Species of the polyomavirus genus.";
VIROLOGY 143:196-211(1985).
-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 72 ICOSAHEDRAL UNITS, EACH OF WHICH IS COMPOSED OF FIVE COPIES OF VPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; POLYOMAVIRUS.
                                                                                                                                                                     FAMILY; COLLAGEN
         entities 1. entities 1. entities 1. entities 2. entites 2.
                                                                                                                                                                                                                                                                                                                                                                           Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1; Length 368; Pred. No. 5.86e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches 10; Indels
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01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
03T PROTEIN VP1.
LYMPHOTROPIC POLYOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Local Similarity 32.0%; Pred. No.
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1 RPGPPGLQGRLQRLLQANGNHAAGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00718; Polyoma_coat; 1. HSSP; P49302; 1SIE. LATE PROTEIN; COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40211 MW;
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                                                                                                                                                                                                                                                                                                                                                                           32.3%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PGPPGLQGRLQRLLQANG 19
                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 AA;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 86045879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1986 (REL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COA1_POVLY
P04010;
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                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
PAULEY A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
-!- SUBMINIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE SONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification, sequence and expression patterns of the Caenorhabditis elegans col-36 and col-40 collagen-encoding genes."; GENE 137:281-285(1993).
  FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 1; Length 398;
Pred. No. 4.07e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CUTICLE COLLAGEN 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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                                                                                                                                                                                                               SUBUNIT: BINDS DNA AS A DIMER.
                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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1 RPGPPGLQGRLQRLLQ 16
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STRAIN=BRISTOL N2;
MEDLINE; 94131298.
LEVY A.D., KRAMER J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                   REPLICATION.
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cDNA for proteinase 3: a serine protease, antibiotic, and from human neutrophils.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BORIES D., RAYNAL M.-C., SOLOMON D.H., DARZYNKIEWICZ Z., CAPRE Y.E., "Down-regulation of a serine protease, myeloblastin, causes growth arrest and differentiation of promyelocytic leukemia cells."; CELL 59:959-968(1989).
BURKHART-SCHULTZ K.J., GORDON L., KYLE A., RAMIREZ M., STILWAGEN S., PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J., DANGANAN L., POUNDSTONE P., CRRISTENSEN M., GEORGESCU A., AVILA J., LUU S., ATTIX C., ANDREISE T., TRANKHEIM M., AMICO-KELLER G., COEFTELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S. SUBMITLER B., OLSEN A.S., CARRANO A.V.; SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                           CAMPANELLI D., MELCHIOR M., FU Y., NAKATA M., SHUMAN H., NATHAN C., GABAY J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 28-48, AND IDENTITY OF WEGENER'S AUTOANTIGEN WITH PR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Three human elastase-like genes coordinately expressed in the myelomonocyte lineage are organized as a single genetic locus on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Three human elastase-like genes coordinately expressed in the myelomonocyte lineage are organized as a single genetic locus
                                                                                                                                                                                              SEQUENCE OF 2-256 FROM N.A., AND SEQUENCE OF 48-71 AND 156-181 MEDLINE; 91079774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Structural and functional properties."; J. BIOL. CHEM. 266:9540-9548(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GABAY J.E., SCOTT R.W., CAMPANELLI D., GRIFFITH J., WILDE C., MARRA M.N., SEEGER M., NATHAN C.F.; "Antibiotic proteins of human polymorphonuclear leukocytes."; PROC. NATL. ACAD. SCI. U.S.A. 86:5610-5614(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIMMER M., MEDCALF R.L., FINK T.M., MATIMANN C., LICHTER P.,
JENNE D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JENNE D.E., ISCHOPP J., LUEDEMANN J., UTECHI B., GROSS W.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAO N.V., WEHNER N.G., MARSHALL B.C., GRAY W.R., GRAY B.H., HOIDAL J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIMMER M., MEDCALF R.L., FINK T.M., MATIMANN C., LICHTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUPTA S.K., NILES J.L., MCCLUSKEY R.T., ARNAOUT M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY OF WEGENER'S AUTOANTIGEN WITH PROTEINASE MEDLINE; 91055123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROC. NATL. ACAD. SCI. U.S.A. 89:8215-8219(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROC. NATL. ACAD. SCI. U.S.A. 89:8215-8219(1992).
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                                                                                                                                                                                                                                                                                                                              EXP. MED. 172:1709-1715(1990).
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                                                                                                                                                                                                                                                                                                            autoantigen
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01-APR-1990 (REL. 14, CREATED)
115-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3)
PRIN3 (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                        MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
"MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
"Molecular cloning and characterization of murine interleukin-11.";
EXP. HEMATOL. 24:1369-1376(1996).

1-FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOWA PROLIFERATION,
T.CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
CELLS AND SYNERGIZES WITH IL-3 IN SUPPORTING MURINE
MEGARARROCYTE COLONY FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                             IL11.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
LAMERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 92021028.
LABBAYE C., MUSETTE P., CAVRE Y.E.:
"Wegener autoantigen and myeloblastin are encoder PROC. NATL. ACAD. SCI. U.S.A. 88:9253-9256(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 1; L
Pred. No. 8.40e+00;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKIN-11.
                                                                                                                                                                                        01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
                                                                                                                                                   199 AA
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                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03421; G415654; -.
MGD; MGI:107613; IL11.
CYTOKINE; GROWTH FACTOR; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.8%;
ilarity 53.3%;
Conservative
                        PVQLQGRLERLIKS 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 PELGALQARLERLLR 138
                                                                                                                                                     STANDARD;
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PGPPGLQGRLQRLLQ 16
                                                               4 PPGLQGRLQRLLQA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 1
199 AA;
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 97070356.
                                                                                                                                                IL11_MOUSE
P47873;
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SEQUENCE

SIGNAL

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Query Match

Best Loca Matches

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protein - protein database search, using Smith-Waterman algorithm MasPar time 4.86 Seconds 122.505 Million cell updates/sec MPsrch\_pp

Fri Aug 20 21:20:36 1999; Run on:

Tabular output not generated.

(1-28) from USO8938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28 >US-08-938-548B-12 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 15 Scoring table:

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseq35 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 39:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

scale 0.251 Variance 88.282; Mean 22.192; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	•	,															
	Pred. No	2.26e-11	2.26e-11	2.26e-11	2.26e-11	2.79e-10	6.37e+01	6.37e+01	9.27e+01	1.12e+02	1.12e + 02	1.12e + 02	1.34e+02	1.34e+02	1.34e+02	1.34e+02	1.34e+02
	Description	Mouse HFGAN72 recepto	Rat HFGAN72 receptor	Mouse hypocretin 35.	Rat hypocretin 35.	Human HFGAN72 recepto	LexA/NuMA fusion prot	GAL4/HA/NuMA fusion p	"p33" N-terminal (2).	Retinoid X receptor i	Human recombinant col	Protein (OA-519) cros	Deduced sequence of h	MY17 preproPR-3.	KM31-7 precursor.	Human KM-102-derived	S. cerevisiae scaur2R
SUMMARIES	01	W61383	W61382	W50158	W50157	W61381	W21732	W21731	R20235	R99737	W68485	W32881	R45403	R85639	R92050	W83404	R67691
	DB	33	33	30	30	33	23	23	4	18	35	24	σ	15	16	38	13
	% Query Match Length DB	123	130	130	130	131	2192	2272	10	716	1464	2509	256	256	549	551	1477
	& Query Match	100.0	100.0	100.0	100.0	94.5	33.8	33.8	32.8	32.3	32.3	32.3	31.8	31.8	31.8	31.8	31.8
	Score	201	201	201	201	190	68	68	99	65	65	65	64	64	64	64	64
	Result No.	н	2	m	4	S	Ø	7 .	ω	თ	10	11	12	13.	14	15	16

Mouse HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure;
HFGAN72 receptor; eating disorders; renal disease; heart failure;
exual dystunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder. 33..65 /note= "Ligand 72A" 69..96 /note= "Ligand 72B" Location/Qualifiers standard; Protein; 123 AA. 02-OCT-1998 (first entry) 17-DEC-1997; 310216. 26-SEP-1997; US-939093. 17-DEC-1996; US-033604. 19-MAR-1997; US-820519. 02-UUL-1997; US-887382. EP-849361-A2 Key Region Mus sp. Region 

(SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI; 98-324672/29.

HFGAN72 receptor ligands - and corresponding DNA, agonists

antibodies, antagonists, etc.

Claim 5: Fig 5: 35pp; English.

The HFGANT2 receptor protein contains two ligans whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGANZ receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, Parkinson's disease, both acute and congestive heart failure, hypotension, hypertension, urieary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign

Location/Qualifiers

¥.

(first entry)

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NIP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
                T 6
W21732 standard; Protein; 2192.
W21732;
                                                                               LexA/NuMA fusion protein.
                                                                                                                                              Homo sapiens.
                                                           01-0CT-1997
                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                         protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HrGAN72 receptor ligands - and corresponding DNA, agonists,
antibodies, antagonists, etc.
Claim 2: Fig 2: 35pp; English.

The HrGAN72 receptor protein contains two ligands whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HrGAN72 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1, or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, parkinson's disease, both acute and congestive heart failure, hypotension, hypotension, uninary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired clisoners tolerance, sexual dysfunction and psychotic and neurological disorders including anxiety, schizophrenia manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's constants.
                                                                                                                                                                                                                                                                                                                               Human HFGAN7 receptor protein.

HFGAN72 receptor; eating disorders; renal disease; heart failure;

HFGAN72 receptor; eating disorders; renal disease; heart failure;

Sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;

Osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;

neurological disorder.
                                                                                                                                                             ö
                                                                                                                                                           Gaps
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect
                             the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor. Sequence 130 AA;
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0
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Pred. No. 2.79e-10;
2; Mismatches 0; Indels
                                                                                                                              Length 130;
                                                                                                            Score 201; DB 30; Length 13.
Pred. No. 2.26e-11;
'''...a+rhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SWITHKLINE BEECHAM CORP.

(SMIK ) SMITHKLINE BEECHAM PLC.

Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI: 98-124672/29.

N-PSDB; V28138.
                                                                                                                                                                                          69 rpgppglqgrlqrllqangnhaagiltm 96
                                                                                                                                                                                                                      1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28
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/note= "Ligand 72A"
70..97
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/note= "Ligand 72B"
                                                                                                                                                                                                                                                                                  W61381 standard; Protein; 131 AA. W61381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 94.5%;
Local Similarity 92.9%;
nes 26; Conservative
                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
les 28; Conservative
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-1997; US-939093.
17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1998.
17-DEC-1997; 310216
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                    02-0CT-1998
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In draywords.

The sequences given in W21731-32 represent fusion proteins which contain The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitoria apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
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                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding nuclear mitotic appts, interacting proteins - useful for modulating cell division and proliferation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 23; Length 212.
Pred. No. 6.37e+01;
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/label= Residues_18-2116_of_NuMA
365..1864
/label= Colled_coil_region
                                                                                                      /label= Residues_18-2116_of_NuMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..147
/label= GAL4_DNA_binding_domain
1..87
/label= LexA_DNA_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Hemaglutinin_epitope
                                                                                                                       285..1784
/label= Coiled_coil_region
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                                          88..94
/label= Polylinker
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GAL4/HA/NUMA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%;
50.0%;
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                                                                                                                                                                                                                                                                           Snyder MP;
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                                                                                   .2192
                                                                                                                                                                                                                                US-478408.
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                                                                                                                                                                                 19-DEC-1996.
07-JUN-1996; U09504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2192 AA;
                                                                                                                                                                                                                                                                       McPherson SMG, Sny
WPI; 97-077270/07.
                                                                                                                                                                                                                              07-JUN-1995; US-47
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                  N-PSDB; T77783
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                                                                                                                                                                                                                                                                                                                                                                           diagnosis
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Best Loca Matches

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                                                                                                                                                                                                                                                                                 Constructed from a long and the ITST 128.0 bp of cocding sequence, whereas clone alpha22 contained sequence encoding amino acids 171-1454 of the protein and around 500 bp of the 3' untranslated region. The 2 clones were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing TAA upstream of the sequence encoding the PRS (Dathogenesis-related protein S) signal peptide and bases 66-77 from the sequence encoding the N-terminus of the pro-collagen amino propeptide domain. (C) the whole of the amino propeptide domain (nt 72-479); (D) all of the amino-telopeptide domain (nt 474-534) and the N-terminus of the elicoidal region (nt 535-1920); (B) the DraIII-BamHI fragment (1709-2808) of alpha22, encoding as 567-936 of the central helicoidal comain. (F) the BamHI-EcoRI (2803-4362) region of alpha22, encoding as 936-1192 in the central helicoidal domain and as 1193-1461 and also including the KDEL motif for retention in the ER. This sequence constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (A), (D), (E), (F) and (G). The recombinant constructed from fragments (C) as prostheses for extracts and parts are useful as biomaterials (C) as prostheses for cardiac valves, ligaments or tendons; skin substitutes; approaches the encoding and parts (C) and (G) as prostheses for cardiac valves, ligaments or tendons; skin substitutes; approaches and parts (C) and (G) and parts (C) and (G) and parts (
Disclosure; Fig 7; 138pp; French. The invention of mammalian collagen in plants. The invention relates to the production of mammalian collagen in plants. 2 clones: alpha3 and alpha22, spanning the human collagen type I gene were isolated from a MG-63 osteosarcoma library. Clone alpha3 contained 83 bp of the 5' untranslated region and the first 1920 bp of coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticancer agents or anti-inflammatories; surgical thread and components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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OA-519; cross-reaction; haptoglobin related; hpr; antibody;
epitope; haptoglobin 1; haptoglobin 2; cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 35; Length 1464;
Pred. No. 1.12e+02;
1; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produce glues, surgical prostheses and foods.
Sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W32881 standard; Protein; 2509 AA.
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24-JAN-1989; US-188426.
17-JAN-1989; US-297722.
04-DEC-1990; US-297722.
26-JUL-1991; US-735522.
24-JUL-1992; US-91716.
05-JUL-1993; US-091716.
05-JUL-1995; US-091716.
05-JUL-1995; US-091716.
05-JUL-1995; US-091716.
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WPI; 97-469516/43.
N-PSDB; T88206.
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Best Local Similarity 64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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ص
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             \begin{smallmatrix} \mathbf{A} & \mathbf{B} & \mathbf{B}
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Trom its precursor - identified using TNF convertase, e.g.

from its precursor - identified using TNF convertase, e.g.

from its precursor - identified using TNF convertase, e.g.

mutchin(s), antibodies or peptide phosphonate(s), for preventing

mutchin(s), antibodies or peptide phosphonate(s), for preventing

Disclosure; Fig 2; 69pp; English.

ProTNF refers to TNF having a molecular weight of about 26,000,

which is the prohomone form of TNFa. ProTNF is cleaved to a lower

molecular weight 'mature' form, pref. 17kD, which, in its multimeric

(usually trimeric) form, is substantially involved in producing life-

threatening physiological changes associated with sepsis. ProTNF is

cleaved by convertase. One TNF convertase is serine protease

proteinase-3, also called PR-3, P-299 or myeloblasin. A suitable

source of convertase is the HL60 cell line (or extracts, or the

culture media in which it is grown). The convertase produced by

Culture media in which it is grown). The convertase produced by

serine protease PR-3 which has other activities unrelated to TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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MX17 preproPR-3.
PR-3; preproPR-3; MX17; human neutrophil protease-3; serine protease; tumour necrosis factor alpha; TNFalpha; HL60; MX17; B Cell; T cell; tumour necrosis factor alpha convertase; cytokine; septic shock; rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease; ischamia/reperfusion injury; autoimmune disease; AIDS.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                        ដ
Claim 2; Columns 43-60; 68pp; English.#
The present sequence is a protein (QA-519) cross-reactive with the haptoglobin related (hpr) gene product. OA-519 can be used raise antibodies reactive with epitopes found on the hpr gene product, but not on haptoglobin 1 or 2, useful in cancer, especially breast cancer, prognosis assays.
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                                                                                                                                                                                                                                                   Length 2509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           convertase; proteinase-3; PR-3; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 256;
                                                                                                                                                                                                                                                   Score 65; DB 24; Length 250 Pred. No. 1.12e+02; 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1992; US-905546.
(CETU ) CETUS ONCOLOGY CORP.
Halenbeck RF, Jewell DA, Koths KE, Kriegler M, Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.8%; Score 64; DB 9; Length 256; larity 38.5%; Pred. No. 1.34e+02; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-1994 (first entry)
Deduced sequence of human proteinase-3 (PR-3)
                                                                                                                                                                                                                                                                                                                                                                           411 ppapaphatlprllrasgrtpeavqkl 437
                                                                                                                                                                                                                                                                                                                                                                                                                                        PGPPGLQGRLQRLLQANGNHAAGILTM 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 256 AA
                                                                                                                                                                                                                                                   Query Match 32.3%;
Best Local Similarity 29.6%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halenbeck RF, Jewe
WPI; 94-026195/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9400555-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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Best Local S
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                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 12
R45403 s
R45403;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:24:10 1999; MasPar time 1.85 Seconds 153.946 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

106580 seqs, 10152877 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 20.582; Variance 81.576; scale 0.252 Statistics:

# SUMMARIES

Pred. No.	2.72e+01	2.72e+01	2.72e+01	2.72e+01	3.30e+01	4.00e+01	4.00e+01	5.87e+01	7.10e+01	8.57e+01	8.57e+01	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02
g	, Applicatio	1, Applicati	, Applicatio	2, Applicati	, Applicatio	, Applicatio	.0, Applicati	, Applicatio	', Applicatio	, Applicatio	., Applicatio	', Applicatio	, Applicatio	', Applicatio	, Applicatio	, Applicatio	, Applicatio	', Applicatio	.4, Applicati	, Applicatio	.4, Applicati	, Applicatio	, Applicatio
Description	Sequence 4	Sequence 1	Sequence 5	Sequence 1	Sequence 3	Sequence 4	Sequence 1	Sequence	Sequence 2	Sequence 3	Sequence 1	Sequence 2	Sequence 4	Sequence 2	Sequence 8	Sequence 4	Sequence 4	Sequence 2	Sequence 1	Sequence 4	Sequence 1	Sequence 4	Sequence 4
ID	US-08-363-	US-08-363-	US-08-363-	US-08-363-	PCT-US91-0	PCT-US95-1	US-08-469-	US-08-804-	US-08-494-	US-08-858-	US-08-858-	PCT-US93-0	US-07-949-	US-08-115-	US-08-792-	US-08-814-	US-08-017-	US-07-941-	US-07-921-	PCT-US93-0	PCT-US94-1	US-08-115-	US-07-941-
DB	7	7	~	~	m	m	Н	~	Н	7	~	m	Н	-	Н	~	Н	Н	-	m	m	Н	Н
% Query Match Length DB	442	442	445	445	10	716	2509	1841	1694	381	381	199	199		199			199	296	296	296	296	296
% Query Match	33.3	33.3	33.3	33.3	32.8	32.3	32.3	31.3	30.8	30.3	30.3	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9
Score	49	67	67	67	99	65	65	63	62	61	61	9	9	9	09	09	9	9	9	09	9	09	09
Result No.	1	7	æ	4	5	9	7	∞	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1. 03 e+02 1. 05 e+02 1. 25		
Sequence 14, Application Sequence 10, Application Sequence 2, Application Sequence 3, Application Sequence 3, Application Sequence 6, Application Sequence 6, Application Sequence 16, Application Sequence 16, Application Sequence 16, Application Sequence 16, Application Sequence 10, Application S	, h. fe.	255 -20002.22
296 1 US-08-165- 300 2 US-08-744- 405 1 US-07-745- 405 1 US-07-745- 405 1 US-07-768- 405 1 US-08-768- 530 2 US-08-363- 530 2 US-08-363- 530 2 US-08-363- 530 2 US-08-363- 116 2 US-08-816- 116 2 US-08-816- 116 2 US-08-816- 116 2 US-08-816- 116 2 US-08-816- 117 3 PCT-US96-1 176 2 US-08-816- 176 2 US-08-816- 176 2 US-08-816- 176 2 US-08-816- 136 4 549-860-2 226 4 549-860-2	PRT 1.00%	8/363, 430 25237 0N:
000000000000000000000000000000000000000	3-255-4 4, App. 6, App. 10. INFORT. 11. INFORT. 12. INFORT. 13. INFORT. 14. INFORT. 15. INFORT. 16. INFORT. 17. IN	APPLICATION NUMBE FILING DATE: 23- CLASSIFICATION: TORNEY/AGENT INFO NAME: MONROY, GI REGISTRATION NUM REFERENCE/DOCKET LECOMMUNICATION: 1 TELEFAX: (415) 4 TELEFAX: 706141 RMATION FOR SEQ 1
4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SULT 1 US-08-36 XXXXXX Sequence Sequence Patent GENERA APPL APPL APPL APPL APPL APPL APPL AP	A ATIO
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Score 65; DB 1; Length 2509;
Pred. No. 4.00e+01;
10; Mismatches 9; Indels
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Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Rolbstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                          1841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
                                                                                                                                         ANTI-SERSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
JENCE 2509 AA; 273089 MW; 32011381 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 1841 AA; 191190 MW; 14819276 CN;
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                  411 PPAPAPHATLPRLLRASGRTPEAVOKL 437
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08804227C
                                                                                                                                                                                                                                                                 2 PGPPGLQGRLQRLQANGNHAAGILITM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: x =
TELECOMMUNICATION INFORMATION:
                                               INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 317-276-2459 INFORMATION FOR SEQ ID NO: 6:
                                                                       LENGTH: 2509 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1841 amino acids
          TELEFHONE: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                            ESS: single
linear
                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                    Query Match 32.3%;
Best Local Similarity 29.6%;
Matches 8; Conservative
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3Y: unknown
                                                                                 TYPE: amino acid
STRANDEDNESS: si
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US-08-804-227C-6
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Pred. No. 4.00e+01;
7; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08469005A
Patent No. 5665874
GENERAL INFORMATION:
APPLICANT: KUHADJA, FRANCIS P.
APPLICANT: PASTERNACK, GARY A.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
FILING DATE: 05-UUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
RIANG APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
                                                                                 00786/246001
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REFERENCE/DOCKET NUMBER: 062482-0113
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                               MOLECULE TYPE: DNA
SEQUENCE 716 AA; 80130 MW; 2569266 CN;
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 24-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08469005A
                    APPLICATION NUMBER: 08/372,652
ATORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-5070
TELEFX: 200154
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Posorske, Laurence H
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                               621 QGRLLSLLEQSEHRTTGV 638
                                                                                                                                                                                                                                                 32.3%;
Local Similarity 38.9%;
Les 7; Conservative
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Sequence 3, Application US/08858052
Patent No. 5849498
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Gueglar, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Nell C.
TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTRUL-COENZYME A
TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTRUL-COENZYME A
CORRESPONDENCES:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                        Sequence 3, Application US/08858052
                                                                                                                                                                                                                              Palo Alto
                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                STREET: 317.
CITY: Palo STATE: CA
COUNTRY: US.
ZIP: 94304
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                                                                                                                                                                                                                                                            APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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Pred. No. 7.10e+01;
0; Mismatches 1; Indels
 Length 1841;
                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                          1694 AA.
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 Score 63; DB 2; L. Pred. No. 5.87e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 40397/104/BABR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 1694 AA; 165283 MW; 14956750 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                        Sequence 2, Application US/08494168
Patent No. 5731192
GENERAL INFORMATION:
                                                                                                                                                                                                   Sequence 2, Application US/08494168
                                                1513 RDTPAALAAHLAELLATARDHGPG 1536
                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1694 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                          STANDARD;
Query Match 31.3%;
Best Local Similarity 33.3%;
Matches 8; Conservative
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Local Similarity 88.9%;
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US-08-858-052-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,052
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 2; Lend
Pred. No. 8.57e+01;
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CLONE: 1575573
KCE 381 AA; 42837 MW; 742169 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08858052
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPPGLOGRLORLLOANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION TELECOMMUNICATION TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                   : 381 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 30.3%;
Local Similarity 26.9%;
les 7; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Patent No. 5437863
CENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
CORRESPONDENCE ADDRESS:
ADDRESSEET: Pennsylvania
                                                                                                                                         ö
                                                                                                                      Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/941,372
ATTOREY/ACENT INFORMATION:
AND APPLICATION NUMBER: US 07/941,372
ATTOREY/ACENT INFORMATION:
                                                                                                                                                                                                                199 AA.
                                                                                                                 29.9%; Score 60; DB 1; L. Similarity 70.0%; Pred. No. 1.03e+02; 7; Conservative 3; Mismatches 0
     ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTARATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: 5174BPCT
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                         MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                      Sequence 2, Application US/08115680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                 STANDARD;
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                             Local Similarity
                                                                                                                                                         129 LQARLDRLLR 138
                                                                                                                                                                           7 LOGRIQRILO 16
                                                                                                                                                                                                                                                                                                                                                                                                                     19477
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                                                                                                  SEQUENCE
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Patent No. 5741772
Patent No. 5741772
Patent No. 5741772
Patent No. 5741772
Patent No. 5741773
Paplicant: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDERS: ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

21P: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 31
ATTONEV/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31.602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
**NWCTH: 199 amino acids
    Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 1; Length 199;
Pred. No. 1.03e+02;
3; Mismatches 0; Indels
  Score 60; DB 1; Length 199;
Pred. No. 1.03e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                   199 AA
                                                                                                                                                                                                     PRT;
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199 AA; 21429 MW; 188641 CN;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:21:48 1999; MasPar time 4.63 Seconds 242.105 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

Database:

Mean 30.698; Variance 52.943; scale 0.580 pir60 1:pir1 2:pir2 3:pir3 4:pir4 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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S61858 A46101 B46101 RDYCS7 S27812 A43917 S64616 S64616 A42115 A42115 A42115 A42115 A42115 A42115 A42115 A42105 A4	ALIGNMENT	type comple protein T9 Arabidopsi	equence_r	; Lin, X. .; Sykes, .R.; Adam	e EMBL D liana ch	ary; trans label ROU AC002505;	/2; 123, molecul	Score 7 Pred. N 8; Mi	DS 138	: AG 24	ype comple smutase (E	parainfluenzae Haemophilus par sequence_revisi	angford, (1991) 17
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                                                                                                                                                            Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence not shown; translation not shown
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hypothetical protein F22013.25 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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#length 879 #molecular-weight 96834 #checksum 5911
              H64888 #type complete
membrane protein ydbH - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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#length 1015 #molecular-weight 111751 #checksum 6299
                                                                                                                                                                                                                                                               #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
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Pred. No.
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##residues 1-879 ##label BLAT
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larity 50.0%;
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Bolothin, A.; Borchert, S.; Borrish, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Borusillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
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S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi,
G.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.;
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M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
W.; Pohly T.M.; Poritelelle, D.; Rapoport, G.;
Rey, M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
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Takemaru, K.; Takeuni, M.; Tamakoshi, A.; Tanaka, T.;
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Wambutt, R.; Wanhier, F.; Vasdiler, H.; Manhutt, R.; Wanhutt, R.; Wanler, E.; Wanller, H.; Wanhutt, R.; Wanhutt, R.; Wanler, E.; Wanller, M.; Wanhutt, R.; Wanhutt, R.; Wandler, E.; Wanller, M.; Want, M.; Wanhutt, R.; Wandler, E.; Wanller, M.; Wanner, F.; Vasdiler, M.; Wanner, E.; Wandler, E.; 
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Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
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                                                                                                                                                                                                                                                               #authors Yang, C.H.; Lambie, E.J.; Snyder, M.
#journal J. Cell Biol. (1992) 116:1303-1317
#title Numba: an unusually long coiled-coil related protein in the mammalian nucleus.
#cross-references MUID:92176231
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                            NuMA protein - human
#formal_name Homo sapiens #common_name man
19.Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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#type complete
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##residues 1-2115 ##label YAN
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Best Local Similarity 50.0%;
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##molecule_type DNA
##resid
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REFERENCE
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                                                                       *superfamily Streptomyces transcription initiation factor sigma; transcription initiation factor sigma katF homology DNA binding; sigma factor; transcription initiation
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#journal Gene (1992) 122:63-70
#title Four genes in Streptomyces aureofaciens containing a domain
characterstic of principal sigma factors.
#cross-references WUID:93083996
                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces aureofaciens
#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
17-Mar-1999
                                                                                                                                             #domain transcription initiation factor sigma katF
homology #label KTF
#length 525 #molecular-weight 57204 #checksum 9676
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homology #label KTF
#length 528 #molecular-weight 57598 #checksum 7360
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#formal_name Pichia pastoris
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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J. Cell Biol. (1994) 127:1259-1273
Role of the PASI gene of Pichia pastoris in peroxisome
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##residues 1-528 ##label KOR
##cross-references GB:M90412; NID:g153308; PID:g153309
   ##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:g153305; PID:g153306
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Pred. No. 7.06e+00;
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#cross-references MUID:95050987
#accession A55152
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Best Local Similarity 31.8%;
Matches 7; Conservative
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Best Local Similarity 36.4%;
Matches 8; Conservative
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Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P. Lumm, W.; Pothier, B.; Qlu, D.; Spadafora, R.; Vicaire, R. Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso, A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.; Pietrokyski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
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deoxyuridine 5-triphosphate nucleotidohydrolase related
protein - Methanobacterium thermoautotrophicum (strain
Delta H)
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Jun-1998
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                                                                                                                                                                                                                                                                                                                                             #checksum 2540
                                                                                                                                                                                                                           #region nucleotide-binding motif A (P-loop)\
#domain FtsH/SEC18/CDC48-type ATP-binding domain
homology #label VATP.
#region nucleotide-binding motif A (P-loop)
#length 1157 #molecular-weight 126983 #checksum 2540
                                                                                                               #superfamily FtsH/SEC18/CDC48-type ATP-binding domain
homology
ATP; P-loop; peroxisome biogenesis
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Complete genome sequence of Methanobacterium
thermoautotrophicum Delta H: functional analysis
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Best Local Similarity 60.0%; Pred. No. 7.06e+00;
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Pred. No. 9.90e+00;
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#cross-references MUD:98037514
#accession D69081
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Best Local Similarity 50.0%;
Matches 9; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:22:38 1999; MasPar time 3.26 Seconds 242.897 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.574; Variance 48.443; scale 0.652

### SUMMARIES

Pred. No.
Description
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DB
Length
% Query Match
Score
Result No.

31.3 878 1 ECR_DROME ECDYSONE RECEPTOR (ECD 1.20e+01 30.8 11 Y310_HUMAN HYPOTHETICAL 28.7 KD P 1.70e+01 30.8 380 1 F812_MOUSE FACTOR VII INTRON 22 1.70e+01 30.8 40.1 ASSY_SYNP3 ARGININGSUCCINATE SYNT 1.70e+01 30.8 684 1 CALH_HUMAN COLLAGEN ALPHA 1(XVIII 1.70e+01 CAA4_HUMAN COLLAGEN ALPHA 6[IV) C 1.70e+01 30.8 1678 1 CAA4_HUMAN COLLAGEN ALPHA 6[IV) C 1.70e+01 30.8 1758 1 CAA4_HUMAN COLLAGEN ALPHA 2[IV) C 1.70e+01 30.8 1763 1 CAA4_ACSU PROCOLLAGEN ALPHA 2[IV) C 1.70e+01 30.8 1763 1 CAA4_ACSU PROCOLLAGEN ALPHA 2[IV) C 1.70e+01 30.3 134 1 Y652_METJA HYPOTHETICAL PROTEIN D 2.41e+01 30.3 22 1 BASR_SALTY TRANSCRIPTICAL CAIDOREDU 2.41e+01 30.3 374 1 RGSX_BOVIN RETINA SPECIFIC REGULA 2.41e+01 30.3 374 1 RGSX_BOVIN RETINA SPECIFIC REGULA 2.41e+01 30.3 516 1 LEGBGOSHI LEGUMIN B PRECURSOR (B 2.41e+01 30.3 518 1 BARZ_SCHCO PROBABLE DNA PACKAGING 2.41e+01 4VIER_EBV PROBABLE DNA PACKAGING 2.41e+01 4VIER_EBV PROBABLE DNA PACKAGING 2.41e+01	ALIGNMENTS	STANDARD; PRT; 187 AA.	P25842; 01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 27, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1).	S PARAINFLUENZAE. PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE; S.	ROM N.A. 1; 2041655,	, LANGFORD P.R., LOYNDS B.M.; os superoxide dismutase of Haemophilus influenzae and H.	OL. 173:7449-7457(1991). ON: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE AND ARE TOXIC TO PROLOGICAL SYSTEMS	ON: MAY CONFER SURVIVED ADVANTAGES.  ATION OF SUPEROXIDE OF ENVIRONMENTAL ORIGIN TO HYDROGEN DE, DISRUPTIVE TO THE NORMAL MUCOCILIARY CLEARANCE PROCESS	+ 2 H(+) = O(2) + H(2)0	SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL). SIMILARITY: BELONGS TO THE CU-2N SUPEROXIDE DISMUTASE FAMILY.	-PROT entry is copyright. It is produced through a collaboration	tstatic 18 on 1	5 5	13; G148884; 4; B41654.	S00087; SOD_CU_ZN_1; 1. S00332; SOD_CU_ZN_2; 1. 080; sodcu; 1.	46; IYAI. TASE; COPPER; ZINC; PERIPLASMIC; SIGNAL. 1 23 POTENTIAL.	24 187 SUPEROXIDE DISMUTASE [CU-ZN].
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Matches

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                                                                                                                                                                                                                                                           AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIWOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOWURA K., NAKAWURA Y., NARHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                           BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES.J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK D.P.; SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 1; Length 8/9;
Pred. No. 1.94e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; FRANKINEAE; FRANKIACEAE; FRANKIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> L (IN REF. 3).
8BFD7CF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95369734.
HARRIOIT O.T., HOSTED T.J., BENSON D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U36928; -; NOT_ANNOTATED_CDS. ECOGENE; EG13180; YDBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 GVDGRLQAILQAHENELGDFVLHM 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
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879 AA; 96834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000235; G1787646; -.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D90776; G1742260;
D90777; G1742264;
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                                    FROM N.A.
112 / MG1655;
97426617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                    MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995
01-NOV-1995
01-OCT-1996
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   SCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
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                                                           STRAIN-K12
                                                                                                                                                                                                                                                  STRAIN=K12
                                        SEQUENCE
                                                                              MEDLINE;
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PROBABLE).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: PROBABLE TRANSPORTER. COULD BE INVOLVED IN THE IMPORT OF VLCFA-COA SYNTHETASE INTO THE PEROXISOMAL MEMBRANE.-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-BINDING; GLYCOPROTEIN; TRANSMEMBRANE; TRANSPORT; PEROXISOME
                                                                                                                                                                                                                                                                                                                                                                                                          SARDE C.O., THOMAS J., SADOULET H., GARNIER J.M., MANDEL J.L., "CDNA sequence of Aldgh, the mouse homolog of the X-linked
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P52645; P77502; P76855; 01-0CT-1996 (REL. 34, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) HYPOTHETICAL 96.8 KD PROTEIN IN LDHA-TYNA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches 10; Indels
   Indels
   2;
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D373B00E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; L
                                                                                                                                                                               01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADRENOLEUKODYSTROPHY PROTEIN HOMOLOG (ALDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   879 AA
   Mismatches
                                                                                                                                                  736 AA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:99672; ALDCH.
PROSITE; PSO0211; ABC_TRANSPORTER; 1.
PFAM; PF00005; ABC_LTAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 AGIPKMQGRLQELRQILGEAAAPVQPL 730
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   4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                adrenoleůkodystrophy gene.";
MAMM. GENOME 5:810-813(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.8%;
Best Local Similarity 44.4%;
Matches 12; Conservative
 Conservative
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                                                                                                                                                  STANDARD;
                                    289 KPGPSGLQAKLASL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
258
353
493
                                                       TISSUE=FIBROTIC LIVER; MEDLINE; 95201443.
                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
473
507
736 AA;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SEQUENCE
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OPPERE NO SOS CONTRACTOR SOS CONTRAC

Gaps

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RESULT ID YC AC PE DT 001 DT 001 DE HI GN YI OS E

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32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PGPPGLQGRLQRLLQANG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K02562; G333278; -. PIR; A03627; VVVP1L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYMPHOTROPIC POLYOMAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COAT PROTEIN VP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COAl_POVLY
P04010;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ID AE
AC P5
DT 01
DT 01
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                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION. IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH RECARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAULEY A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: NEWATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

-!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
MEDLINE; 94131298.
LEVY A.D., KRAMER J.M.;
"Identification, sequence and expression patterns of the Caenorhabditis elegans col-36 and col-40 collagen-encoding genes.";
GENE 137:281-285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P17383; 1DHM.
EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN SEQUENCE 398 AA; 45450 MW; C9BBOCEO CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 1; Le
Pred. No. 4.07e+00;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
COLT.CLE COLLAGEN 36.
COLT.36 OR C27H5.5.
CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR SUBUNIT: BINDS DNA AS A DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%;
ilarity 56.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X70828; G312096; -. PFAM; PF00508; E2_N; 1. PFAM; PF00511; E2_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 RSPPKGGQSRLRRLIQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RPGPPGLQGRLQRLLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity
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                                                                                                                                                                      REPLICATION.
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P34803;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 86045879.
PAMLITA M., CLAD A., ZUR HAUSEN H.;
"Complete DNA sequence of lymphotropic papovavirus: prototype of a new species of the polyomavirus genus.";
VIROLOGY 143:196-211(1985).
-! SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 72 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF FIVE COPIES OF VPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; POLYOMAVIRUS
                                                                                                                                                                                                                                       FAMILY; COLLAGEN
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                          entiti...

R EMBL; L15418; G289662; -..

R EMBL; L15418; G289662; -..

DR WORMPEP; C27145.5; CE06893; REPEAT; MULTIGENE FAMILY; C...

FT DOMAIN 118 150 TRIPLE-HELICAL REGION.

TOMAIN 157 187 TRIPLE-HELICAL REGION.

TOMAIN 157 187 TRIPLE-HELICAL REGION.

TRIPLE-HELICAL REGION.

194 226 TRIPLE-HELICAL REGION.

TRIPLE-HELICAL REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 5.86e+00;
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HSSP; P49302; 1SIE.
LATE PROTEIN; COAT PROTEIN.
SEQUENCE 368 AA; 40211 MW; 4979282C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-607-1986 (REL. 02, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65;
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MEDLINE; 91055123.
GUPTA S.K., NILES J.L., MCCLUSKEY R.T., ARNAOUT M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-20 FROM N.A. MEDLINE; 92390417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATURE 346:520-520(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89315847
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                                                                                                                                GABAY J.E.; "Cloning of
                                                                                                                                                       autoantigen
                                                                                                                                                                                       SEQUENCE OF
                                                                                                                                                                                                                        JENNE D.E.;
                                                                                                                                                                                                                                                                                        SEQUENCE OF
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MEDLINE; 901
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                                                                                                                                                                                                  MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI3_HUMAN STANDARD; PRT; 256 AA.
P24158; P15637;
O1-APR-1990 (REL. 14, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN).
PRIN3 OR MBN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single mRNA.";
                                                                                                                                                                                                       MEDLINE; 97070356.
MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
"Molecular cloning and characterization of murine interleukin-11.";
EXP. HEMATOL. 24:1369-1376(1996).

1. FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,
T-CELL DEPENDENT DEVELOPMENT OF IMMUNGIOBULIN-PRODUCING B
CELLS AND SYNERGIZES WITH IL-3 IN SUPPORTING WURINE
MEGAKARYOCYTE COLONY FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA,
PRIMATES, CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
LAMERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 199;
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MEDBLINE; 92021028.
LABBAYE C., MUSETTE P., CAYRE Y.E.;
"Wegener autoantigen and myeloblastin are encoded by PROC. NATE. ACAD. SCI. U.S.A. 88:9253-9256(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 1; Le
Pred. No. 8.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
INTERLEUKIN-11.
1CB30772 CRC32;
                                                                                            (REL. 33, CREATED)
(REL. 33, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
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                                                                           199
                                                                           PRT;
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CYTOKINE; GROWTH FACTOR; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21522 MW;
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larity 53.3%;
Conservative
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         1539 PVQLQGRLERLIKS 1552
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                                                                          STANDARD;
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                             PPGLOGRIORLIQA 17
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                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 97070356.
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IL11_MOUSE
P47873;
01-FEB-1996 (
01-FEB-1996 (
01-NOV-1997 (
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loning of cDNA for proteinase 3: a serine protease, antibiotic, and toantigen from human neutrophils.";

EXP. MED. 172:1709-1715(1990). BORIES D., RAYNAL M.-C., SOLOMON D.H., DARZYNKIEWICZ Z., CAYRE Y.E., "Down-regulation of a serine protease, myeloblastin, causes growth arrest and differentiation of promyelocytic leukemia cells."; CELL 59:959-968(1989). WILDE C.G., SNABLE J.L., GRIFFITH J.E., SCOTT R.W.; "Characterization of two azurphil granule proteases with active-site homology to neutrophil elastase."; J. BIOL. CHEM. 265:2038-2041(1990). BURKHART-SCHULTZ K.J., GORDON L., KYLE A., RAMIREZ M., STILWAGEN S., PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J., DANGANAN L., POUNDSTONE P., CRRISTENSEN M., GEORGESCU A., AVILA J., LIU S., ATTIX C., ANDRRIES T., TRANKHEIM M., AMICO-KELLER G., COEFTELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S., SUBMITLER J., OLESN A.S., CARRANO A.V.;
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. : ن SEQUENCE OF 28-48, AND IDENTITY OF WEGENER'S AUTOANTIGEN WITH PR-3. myelomonocyte lineage are organized as a single genetic locus on MEDILINE; 91079774. CAMPANELLI D., MELCHIOR M., FU Y., NAKATA M., SHUMAN H., NATHAN ö expressed in the in the SEQUENCE OF 2-256 FROM N.A., AND SEQUENCE OF 48-71 AND 156-181 "Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Structural and functional properties."; J. BIOL. CHEM. 266:9540-9548(1991). GABAY J.E., SCOTT R.W., CAMPANELLI D., GRIFFITH J., WILDE C., MARRA M.N., SEEGER M., NATHAN C.F., "Antibiotic proteins of human polymorphonuclear leukocytes."; PROC. NATL. ACAD. SCI. U.S.A. 86:5610-5614(1989). locus ZIMMER M., MEDCALF R.L., FINK T.M., MATIMANN C., LICHTER P., JENNE D.E., TSCHOPP J., LUEDEMANN J., UTECHT B., GROSS W.L.; "Wegener's autoantigen decoded."; ZIMMER M., MEDCALF R.L., FINK T.M., MATIMANN C., LICHTER P., RAO N.V., WEHNER N.G., MARSHALL B.C., GRAY W.R., GRAY B.H. expressed myelomonocyte lineage are organized as a single genetic IDENTITY OF WEGENER'S AUTOANTIGEN WITH PROTEINASE 3. PROC. NATL. ACAD. SCI. U.S.A. 89:8215-8219(1992). PROC. NATL. ACAD. SCI. U.S.A. 89:8215-8219(1992) Three human elastase-like genes coordinately Three human elastase-like genes coordinately SEQUENCE OF 28-67 AND 228-244. 28-47 AND 196-219. 22-256 FROM N.A. 42-256 FROM N.A.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:23:12 1999; MasPar time 6.52 Seconds 234.276 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQARLQANGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

Searched:

179066 segs, 54579741 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics:

Mean 30.180; Variance 51.706; scale 0.584

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No.	Score	Query	Query Match Length DB	DB	ID	Description	Pred. No.
	201	100.0	130	11	055241	HYDOCKETT / NTERTOROUS	4 746-26
2	201	100.0	130	Ξ	055232	PREPRO-OREXTN	4 746-26
m	197	0.86	131	ဖ	077668	PREPRO-OREXIN PRECIIESO	3.526-25
4	190	94.5	131	4	043612	PREPRO-OREXIN.	1.15e-23
5	16	37.8	1174	9	095168	TIGHT JUNCTION PROTEIN	2.98e-01
9	. 75	37.3	1277	Ξ	035821	PAR INTERACTING PROTEI	4.31e-01
7	73	36.3	249	11	P97382	K+ CHANNEL BETA4 SUBUN	8.98e-01
80	71	35.3	145	10	048721	T9J22.21 PROTEIN.	1.85e+00
σ	70	34.8	511	10	080740	T13D8.6 PROTEIN.	2.64e+00
10	69	34.3	331	13	091640	LEUCINE ZIPPER WITH BA	3.76e+00
11	69	34.3	389	11	088539	WW DOMAIN BINDING PROT	3.76e+00
12	68	33.8	162	7	085680	RNA POLYMERASE SIGMA-L	5.34e+00
13	68	33.8	481	m	042651	HYPOTHETICAL 55.5 KD P	5.34e+00
14	68	33.8	1015	10	064673	F22013.25.	5.34e+00
15	68	33.8	2115	4	014980	NUMA PROTEIN.	5.34e+00
16	67	33.3	161	~	085683	RNA POLYMERASE SIGMA-L	7.55e+00
17	67	33.3	178	~	031955	YONC PROTEIN.	7.55e+00
18	67	33.3	178	σ	064066	HYPOTHETICAL 19.6 KD P	7.55e+00
19	67	33.3	413	11	035141	MAXP1.	7.55e+00
20	67	33.3	462	7	P95644	RNA POLYMERASE SIGMA F	7.55e+00

7.55e+00 7.55e+00 7.55e+00 7.55e+00 7.55e+00 7.55e+00 7.55e+00 1.07e+01 1.0
RNA POLYMERASE SIGMA F HYPOTHETICAL 60.1 KD P ARTICULIN P60.1 KD P CAR. TYAPOTETICAL 41.3 KD P CAR. HYPOTHETICAL AUTIVA TRANSCRIPTIONAL ACTIVA TRANSCRIPTION SYNTHASE (E
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510 511 521 522 528 528 668 668 668 608 130 125 335 335 335 2591 1365 2591 1344 4413 4444 2509
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#### ALIGNMENTS

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TISSUE-BRAIN;
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PAR INTERACTING PROTEIN.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                     BEATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.; "The tight junction protein 20-2 contains three PDZ (PSD-95/Discs-Large/Zo-1) domains and an alternatively spliced
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91084854.
WUMRIN J., SCHIBLER U.;
"Expression of the liver-enriched transcriptional activator protein
DBP follows a stringent circadian rhythm.";
CELL 63:1257-1266(1990).
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                                                                                                                                                                                                                                                            Length 1174;
                                                                                                                                                                                                                                                         Ouery Match 37.8%; Score 76; DB 6; Length 1174 Best Local Similarity 32.1%; Pred. No. 2.98e-01; Matches 9; Conservative 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
COMTE P.A., OSSIPOW V., SCHIBLER U.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                   GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                          EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                       DEACH...
SUBMITTED (AUG-1996) TO EMBL/GENBANN, LL27152; G1536970; -.
EMBL; L27152; G1536970; -.
PFAM; PF00555; PDZ; 3.
PFAM; PF00625; Guanylate_kin; 1.
PFAM; PF00625; Guanylate_kin; 1.
PFAM; PF00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U83590; G2253211; -. SEQUENCE 1277 AA; 144674 MW; 89721F79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA.
                                                                                                                                                                                                                                                                                                                                                                        PRT; 1277 AA
                                                                                                                                                                                                                                                                                                      268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295
                                                                                                 BIOL. CHEM. 271:25723-25726(1996)
                                                                                                                                                                                                                                                                                                                    826 PGAEALHAQVERFVQQAGNQADASVAL 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
 tumor suppressor protein.";
J. CELL BIOL. 124:949-961(1994).
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P97382,
P97382,
O1-MAY-1997 (TREMBLREL. 03, CI
O1-MAY-1997 (TREMBLREL. 03, LZ
O1-NOV-1998 (TREMBLREL. 08, LZ
K+ CHANNEL BETA4 SUBUNIT.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.3%;
Best Local Similarity 29.6%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 91084854.
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                SEQUENCE FROM N.A. MEDLINE; 96421547.
                                                                                         region.";
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035821
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1D P99
AC P99
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARABIDOPSIS THALLANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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VYSOTSKAIA V.S., SCHWARTZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
LIU S., LI J., ARAUJO R., AU M., BRENDEL V., BUEHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURIZ D., LI Y., PALM C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                       MEDLINE; 96421640.
FINK M., DUPRAT F., LESAGE F., HEURTEAUX C., ROMEY G., BARHANIN J., LAZDUNSKI M.;
"A new K+ channel beta subunit to specifically enhance Kv2.2 (CDRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
SOURSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYRES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.,
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC002505; G2739379; -.
SEQUENCE 145 AA; 15355 MW; 660DDF14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                Match 35.3%; Score 71; DB 10; Length 145 Local Similarity 39.1%; Pred. No. 1.85e+00; Local Similarity 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                              8805DBE7 CRC32;
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EMBL; U65593; G1695272; -.
IONIC CHANNEL.
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                            SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                              249 AA; 27749 MW;
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Local Similarity 76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
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01-NOV-1998 (TREMBLREL.
T13D8.6 PROTEIN.
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                                                                        SEQUENCE FROM N.A.
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completed: Fri Aug 20 21:23:53 1999 ne : 41 secs.

1 RPGPPGLQGRLQRLLQAN 18

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01-808-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                   LT 14

064673

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01-AUG-1998 (TREMBLREL. 07, CREATED)

01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

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RABBIDOPSIS THALIANA (MOUSE-EAR CRESS)

EURARYOTA: VIRIDIPLANTAE: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

EUPHYLLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;

CAPPARALES: BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MBDLINES, 92176231.
YANG C.H., LAMBIE E.J., SNYDER M.;
"NUMA: an unusually long coiled-coil related protein in the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
MEDLINE; 94013066.
MAEKAWA T., KURIYAMA R.;
Primary structure and microtubule-interacting domain of the SP-H antiquic Map located at the spindle pole and characterized as a homologous protein to NuMA.";
J. CELL SCI. 105:589-600(1993).
SEMBL; 211583; G35119; -..
CONFLICT 124 124 0 -> P (IN REF. 2).
CONFLICT 124 124 0 -> H (IN REF. 2).
 Gaps
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SHINN P., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN H.,
CONWAY A., CONWAY A., KURTZ D., OJI O., SHEN Y.K., TORLUMI M.,
VINCOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 33.8%; Score 68; DB 10; Length 1015; Best Local Similarity 50.0%; Pred. No. 5.34e+00; Matches 13; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 4; Length 2115;
Pred. No. 5.34e+00;
6; Mismatches 3; Indels
 Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                       ECKER J.R.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC03981; G3063465; -.
SEQUENCE 1015 AA; 111751 MW; 82FA3G3F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499 PTRPGLRSSLKRKRGNNGPTAATILT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PGPPGLQGRLQRLLQANGNHAAGILT 27
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 7;
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Best Local Similarity 50.0%;
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                              280 LQEVLQSDSNHVPSVLT 296
 Conservative
                                             11 LQRLLQANGNHAAGILT 27
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Matches
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:14:33 1999; MasPar time 8.03 Seconds 325.686 Million cell updates/sec on:

Tabular output not generated.

>US-08-938-548B-10 (1-123) from US08938548B.pep

Description: Perfect Score:

Sednence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part14 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Variance 129.928; scale 0.227 Mean 29.551; Statistics:

# SUMMARIES

Query         Query         Description         Pred. No.           1         899         100.0         123         33         W61383         Mouse HFGAN72         1.08e-73           2         894         99.4         130         30         W50158         Mouse HFGAN72         1.08e-73           3         853         94.9         130         30         W50159         Rat hypocretin 35.         2.79e-69           4         853         94.9         130         30         W61382         Rat Hypocretin 35.         2.79e-69           5         734         81.6         131         31         W61382         Rat Hypocretin 35.         2.79e-69           6         113         12.6         400         39         W84186         Glial cell line-deriv 4.05e-01           7         113         12.6         400         39         W84186         Glial cell line-deriv 4.05e-01           8         113         12.6         400         39         W84186         Glial cell line-deriv 4.05e-01           9         113         12.6         400         39         W84186         Glial cell line-deriv 4.05e-01           10         113         12.6         400         39			аP					
100.0 123 33 W61383 Mouse HFGAN12 recepto 1.99.4 130 30 W50158 Mouse hypocretin 35. 3 94.9 130 30 W50157 Rat hypocretin 35. 2 94.9 130 33 W61381 Rat hypocretin 35. 2 94.9 130 33 W61382 Rat HFGAN72 receptor 2.12.6 378 39 W84185 Glial cell line-deriv 4.12.6 400 39 W84186 Glial cell line-deriv 4.12.6 400 39 W65116 Human GDNF alpha-related 1.2.6 400 32 W65117 Human GDNF alpha-3 re 4.12.6 400 32 W65117 Human GDNF alpha-3 re 4.10.7 566 28 W37598 Human fibulin type 1.7 10.7 601 28 R11149 Fibulin A. 10.7 601 28 R11150 Fibulin A. 10.7 601 28 R11150 Fibulin C. 10.7 601 28 W37599 Human fibulin type 1.7 7.001 28 W37599 Human fibulin type 1.7 7.001 28 W37599 Human fibulin C. 10.7 601 28 W37599 Human fibulin R. 10.7 601 28 W37599 Human	Result No.	Score	Query Match	Length	DB	QI QI	Description	Pred. No.
99.4 130 30 W50158 Mouse hypocretin 35. 3. 94.9 130 30 W50157 Rat hypocretin 35. 2. 94.9 130 30 W50157 Rat hypocretin 35. 2. 94.9 130 33 W61382 Rat hypocretin 35. 2. 94.9 131 33 W61381 Human HFGAN72 recepto 6. 12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 32 W65116 Human GDNF alpha-relation 4. 12.6 400 28 W37463 Human GDNF alpha-3 re 4. 12.6 400 28 W37598 Human fibulin type 1. 7. 10.7 566 2 R11148 Fibulin B. 7. 10.7 601 28 R1150 Fibulin B. 7. 10.7 683 2 R11150 Fibulin C.	-	899	100.0	123	33	W61383	Mouse HFGAN72 recepto	1.08e-73
94.9 130 30 W50157 Rat hypocretin 35. 2. 94.9 130 33 W61382 Rat HFGAN72 receptor 2. 81.6 378 39 W84185 Glial cell line-deriv 4. 12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 39 W84180 A GDNFR-alpha-Telated 4. 12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 32 W65117 Human GDNF alpha-3 re 4. 12.6 400 32 W5117 Human GDNF alpha-3 re 4. 10.7 566 2 R11149 Fibulin A. 7. 10.7 601 2 R11149 Fibulin B. 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 W37599 Fibulin C. 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 W37599 Fibulin C.	7	894	99.4	130	30	W50158	Mouse hypocretin 35.	3.25e-73
94.9 130 33 W61382 Rat HFGAN72 receptor 2. 81.6 131 33 W61381 Human HFGAN72 receptor 6. 12.6 400 39 W84185 Glial cell line-deriv 4. 12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 32 W65117 Human GDNF alpha-3 re 4. 12.6 400 28 W37463 Human Ret ligand Ret. 4. 10.7 566 28 R11149 Fibulin A. 7. 10.7 601 28 R11149 Fibulin B. 7. 10.7 601 28 R1150 Fibulin C. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.	m	853	94.9	130	30	W50157	Rat hypocretin 35.	2.79e-69
81.6 131 33 W61381 Human HFGAN72 recepto 6. 12.6 378 39 W84185 Glial cell line-deriv 4. 12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 39 W84180 A GDNFR-alpha-related 4. 12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 28 W37463 Human GDNF alpha-3 re 4. 10.7 556 28 W27598 Human fibulin type 1. 7. 10.7 601 2 R11149 Fibulin B. 7. 10.7 601 28 W37599 Human fibulin type 1. 7. 10.7 601 28 W37599 Human fibulin type 1. 7. 10.7 601 28 R1189 Fibulin B. 7. 10.7 601 28 R1189 Fibulin C. 7. 683 2 R11150 Fibulin C. 7. 7.	4	. 853	94.9	130	33	W61382	Rat HFGAN72 receptor	2.79e-69
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12.6 400 39 W84186 Glial cell line-deriv 4. 12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 32 W7631 Human GDNF alpha-3 re 4. 12.6 400 28 W37463 Human Ret ligand RetL 4. 10.7 566 2 R11149 Fibulin A. 10.7 601 2 R11149 Fibulin B. 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 R11150 Fibulin C.	9	113	12.6	378	39	W84185	Glial cell line-deriv	4.05e-01
12.6 400 39 W84180 A GDNFR-alpha-related 4. 12.6 400 32 W65115 Human GDNF alpha-3 re 4. 12.6 400 28 W77463 Human GDNF alpha-3 re 4. 10.7 556 28 W27598 Human Ret 11gand Ret. 4. 10.7 566 2 R11148 Fibulin A. 10.7 601 2 R11149 Fibulin B. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 R37599 Human fibulin type 1 7. 10.7 683 2 R11150 Fibulin C.	7	113	12.6	400	39	W84186	Glial cell line-deriv	4.05e-01
12.6 400 32 W65116 Human GDNF alpha-3 re 4. 12.6 400 28 W65117 Human GDNF alpha-3 re 4. 12.6 400 28 W37463 Human Ret ligand RetL 7. 10.7 556 28 W37598 Human fibulin type 1 7. 10.7 561 2 R11149 Fibulin B. 7. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 683 2 R11150 Fibulin C.	8	113	12.6		39	W84180	A GDNFR-alpha-related	4.05e-01
12.6 400 32 W65117 Human GDNF alpha-3 re 4. 12.6 400 28 W37463 Human Fet 14gand RetL 4. 10.7 566 2 R11148 Fibulin A. 10.7 601 2 R11149 Fibulin B. 10.7 601 28 W37599 Human fibulin type 1 7. 10.7 601 28 W37599 Fuman fibulin type 1 7. 10.7 601 28 W37599 Fuman fibulin type 1 7.	σ	113	12.6		32	W65116	Human GDNF alpha-3 re	4.05e-01
12.6 400 28 W37463 Human Ret ligand RetL 4. 10.7 556 28 W27598 Human fibulin type 1 7. 10.7 566 2 R11148 Fibulin A. 7. 10.7 601 2 R21149 Fibulin B. 7. 10.7 601 28 W27599 Human fibulin type 1 7. 10.7 683 2 R11150 Fibulin C.	10	113	12.6		32	W65117	Human GDNF alpha-3 re	4.05e-01
10.7 556 28 W27598 Human fibulin type 1 7. 10.7 566 2 R11148 Fibulin A. 7. 10.7 601 2 R11149 Fibulin B. 7. 10.7 601 28 W27599 Human fibulin type 1 7. 10.7 683 2 R11150 Fibulin C. 7.	11	113	12.6		28	W37463		4.05e-01
566 2 R11148 Fibulin A. 7. 601 2 R11149 Fibulin B. 7. 601 28 WA7599 Human fibulin type 1 7. 683 2 R11150 Fibulin C. 7.	12	96	10.7		28	W27598		7.98e+00
601 2 R11149 Fibulin B. 7. 601 28 W27599 Human fibulin type 1 7. 683 2 R11150 Fibulin C. 7.	13	96	10.7		7	R11148		7.98e+00
601 28 W27599 Human fibulin type 1 7. 683 2 R11150 Fibulin C.	14	96	10.7		7	R11149		7.98e+00
683 2 R11150 Fibulin C. 7.	15	96	10.7		28	W27599		7.98e+00
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7.98 e+00 1.86 e+00 1.86 e+00 2.20 e+00 2.20 e+00 2.20 e+00 3.00 e+00	.01e+0
fibulin ty fibulin ty al recombin al recombin N-proteina e human cho N-proteina N-proteina N-proteina N-proteina N-proteina N-proteina A-1BB liga Ophan apore aspartic p napsin A p aglandin A p agrandin A p agrandi	S. clavuligerus ORF1
W27600 W27601 W24783 W24783 W47029 W47029 W47029 W47002 W47002 W75074 W75074 W75082 W77481 W75082 W7	785
228 222 288 333 333 333 333 333 333 333 333 333 3	13
2033 2034 2034 2034 2034 2034 2034 2034	2
00000000000000000000000000000000000000	
00000000000000000000000000000000000000	£
	4.5

# ALIGNMENTS

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Wit; 30-3440.72.

HIGAN72 receptor ligands - and corresponding DNA, agonists,
antibodies, antagonists, etc.

Soliaim 5; Fig 5; 35pp; English.

Claim 5; Fig 5; 35pp; English.

Claim 6; Fig 5; 35pp; English.

Claim 7: The HFGAN72 receptor protein contains two ligans whose antagonists can be consequent to the HFGAN72 receptor protein contains two ligans whose antagonists can be consequent failure, impaired the control of the sexual disease, congestive heart failure, impaired control of the sexual disease, congestive heart failure, impaired treating anorexia nervosa, bulimia and cachexia. The HFGAN72 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, carcer and congestive heart failure, sthma, cachexia, obesity, diabetes, asthma, cachexia, obesity, diabetes, asthma, concentration, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign
                    W61383, 02-0CT-1998 (first entry) Mouse HFGAN72 receptor protein. HFGAN72 receptor protein. HFGAN72 receptor; eating disorders; renal disease; heart failure; sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention; osteoporosis; angina pectoris; myocardial infarction; psychotic disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                 24-JUN-1998.
17-DEC-1997; 310216.
17-DEC-1997; 0S-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
(SMIX ) SMITHKLINE BEECHAM CORP.
(SMIX ) SMITHKLINE BEECHAM PLC.
Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanaqisawa M; WPI; 98-324672/29.
                                                                                                                                                                                                                          33..65
/note= "Ligand 72A"
69..96
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                        /note= "Ligand 72B"
W61383 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                               EP-849361-A2
                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                          Region
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Claim 2; Fig 2: 35pp: English.

Claim 2: Fig 2: 35pp: English.

The HFGAN/2 receptor protein contains two ligands whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bullimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGAN/2 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, Parkinson's disease, both acute and congestive heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired collucose tolerance, sexual dysfunction and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's contracts.
                                                                HFGAN72 receptor ligands - and corresponding DNA, agonists
  Brooks DP, Gellai M, Wilson S, Yanagisawa M;
                                                                                          etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.6%;
Best Local Similarity 81.5%;
Matches 101; Conservative
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25-MAR-1999 (first entry)
                                                                                       antibodies, antagonists,
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/note= "
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20-MAY-1998, U10328.
27-JUN-1997, US-884638.
20-MAY-1997, US-047092.
                       98-324672/29.
                                         N-PSDB; V28138
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                                                                                                                                                                                                                                                                                                                        used for treating obesity, diabetes, anorexia merves, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The agonist is useful for lections to be a section of the action of the action, bypertension, uninary retention, osteoporosis, angina pectoris, myocardial infarction, unlary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired glucose tolerance, excual dysfunction and psychotic and neurological
                                                                                                                                                                                                                                                         antibodies, antagonísts, etc.
Claim 5; Fig 4; 35pp; English.
The HFGAN72 receptor protein contains two ligans whose antagonists can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-ocr-1998 (first entry)

Human HFGAN72 receptor protein.

HFGAN72 receptor; eating disorders; renal disease; heart failure;
sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington' disease or Gilles dela Tourett's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RRPGPPGLQGRLQRLLQRLLQRUGANGNHAAGILTMGRRAGAELEPHPCSGRGCPTVTTTALAPRGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 rrpgppglqgrlqrllqangnhaagiltmgrragaelepypcpgrrcptatalaprgg 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VPWAAVTLILILILPPALLSLGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vpwaavtllllllppallslgvdagplpdccrgktcscrlyellhgagnhaagiltlgk 67
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                                                                                                                                                                                                                                            receptor ligands - and corresponding DNA, agonists,
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                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) BLOOKS DP, Gellai M, Wilson S, Yanagisawa M; WPI; 98-324672/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 853; DB 33;
Pred. No. 2.79e-69;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 34..66 //note "Ligand 72A" 70..97 //note "Ligand 72B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 131 AA.
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al Similarity 95.1%;
117; Conservative
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17-DEC-1997; 310216.
26-SEP-1997; US-939093.
17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
                                     26-SEP-1997; US-939093.
17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
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Matches

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121

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Glial cell line-derived neurotrophic factor receptor gamma 1;
GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gammal
Parkinson's disease; schizophrenia; insomnia; tardive dyskenisla;
hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
renal disorder; kidney failure; gut dysfunction; regeneration;
                                                                                                                                                                                                                       8 vswaavtllllllllppallssgaaaqplpdccrqktcscrlyellhgagnhaagiltlg 67
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                                                      10; Indels 1; Gaps
                                                                                                                                          Score 734; DB 33; Length 131;
Pred. No. 6.74e-58;
12; Mismatches 10; Indels
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Gentz RL, HSu T, Ni J, Ruben SM, Young P;
WPI; 99-070150/706.
N-PSDB; V99333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32..378 //label= mature_protein
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especially tumours.
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       W65116;
28-SEP-1998 (first entry)
28-SEP-1998 (first entry)
Human GDNE alpha-3 receptor protein #1.
Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
muscular dystrophy; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
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Human GDNF alpha-3 receptor protein #2.

Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;

treatment; neurodegenerative disease; Parkinson's Disease; ALS; SNA,

amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;

Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;

muscular dystrophy; diagnostic.
                                                                                                                                                                                                                                                                                                      This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be used to freat e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New factor alpha 3 receptor polypeptide and e.g. DNA and agonists used to treat neuro degenerative diseases, muscular diseases and nerve and muscle trauma and in diagnostic assays claim 13; Fig 4; 22pp; English.
                                                                                                                                                                                                                                                             New factor alpha 3 receptor polypeptide and e.g. DNA and agonists used to treat neuro degenerative diseases, muscular diseases and nerve and muscle trauma and in diagnostic assays claim 4; Fig 2; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 400;
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                                                                                                                                                /note= "Partial sequence"
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                                                                                                                        1..400
/label= GDNF alpha-3
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                                                                                                              Location/Qualifiers
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W65116 standard; Protein; 400 AA
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20-NOV-1997; 309375.
09-MAY-1997; GB-009463.
27-NOV-1996; GB-024677.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                               20-NOV-1997; 309375.
09-MAY-1997; 62-009463.
27-NOV-1996; GB-024677.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.6%;
Best Local Similarity 47.4%;
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                                                                                                                          Protein
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Claim 2: Page 85-86; 113pp; English.

This amino acid sequence comprises human Ret ligand (RetL) RetL3, and clones (see V00251) isolated from a adult heart and spinal cord libraries. Rat and human RetL1, human RetL2 and spinal cord libraries. Rat and human RetL1, human RetL2 and 78 % identical to human RetL3. 34.3% identical to human RetL3. 34.9% identical to human RetL3. 34.9% identical to human RetL3. Set ligand is a key component of the Ret signalling pathway that specifically interacts with Ret receptor protein, triggering Ret dimerisation and/or autophosphorylation of the Ret tyrosine kinase domain.

Wectors containing retL3 DNA and prokaryotic or eukaryotic host and/or autophosphorylation of the Ret tyrosine kinase domain.

Wectors containing retL3 DNA and prokaryotic or eukaryotic host cells transformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and tusion proteins with a toxin, imageable compound or radionuclide.

RetL3, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue,

Particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, moctor neurone disease, multiple sclerosis, bacterial, viral or prion infections (assesse), cranial nerve or spinal cond injury, developmental diseases, untipleral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis).

Fusion proteins are used to deliver toxins etc. to Ret-expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All MAY 1998 (first entry)

Human Ret ligand RetL3.

Ret ligand, RetL3 receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldtd-Jakob disease; caralal nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
myastheria gravis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                               Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                  Score 113; DB 32; Le
Pred. No. 4.05e-01;
9. Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PWAAVTLILLILLILPPALLSLGVDAQPLPDCCRQKTCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 plppvvlmlllllppsplplaa-gdplptesrlmn-sc
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07-MAY-1997.

10-APR-1997, U07726.

10-APR-1996; US-017427.

07-JUN-1996; US-019300.

16-JUL-1996; US-021859.

(BIOJ ) BIOGEN INC.

Cate RL, Hession C, Sanicola-Nadel M;

WPT; 98-018411/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W37463 standard; Protein; 400 AA W37463;
                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.6%;
Best Local Similarity 47.4%;
Matches 18; Conservative
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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

Sclaim 10; Fig 4; 56pp; English.

Claim 10; Fig 4; 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at posm. 566 (terminal codon in fibulin A)

and 683 residues resp. All three forms are rich in cysteine (11 %) and analysis with on. and spacing of the Cys residues revealed two cys repeat moftli (I and II). The type I motif, CC(X)12c-(X)9c10c(X)6cc is repeated twice, separated by an imperfect form of the repeat lacking two Cys residues. The same motif is found in albumin, vitemin D-binding protein and appha-fectportein. The type II motif, related to repeats found in epidermal growth cisulphide stabilized loop structure is thought to be conserved. The type II motif, related to repeats found in epidermal growth cator precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats, (2, 3, 4 and 9) differ from the EGF-IIke motif in having a 4-6 cresidue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence and repeat is a pentapeptide with the consensus sequence XD(I/V)(N)E. Fibulin binds to the cytorylation is abhesion of the cytorylation in the form of the consensus of plasmit of integrin adhesion consensus sequence is betal subunit of integrin adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. See also R11147, R11148 and R11150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human fibulin type 1 isoform (variant B).
Human fibulin protein; met-OB protein; hypertension; obesity;
isoform; type II diabetes; fibrogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ## Watch 10.7%; Score 96; DB 2; Length 601; Local Similarity 57.1%; Pred. No. 7.98e+00; nes 16; Conservative 3; Mismatches 8; Indels
                              'label - consensus pentapeptide
                                                                                                                                                 /label= consensus pentapeptide
                                                                                        consensus pentapeptide
                                                                                                                  /label= repeat unit 8
530..535
                                                          'label = repeat unit 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VTLLLLLLLPPALLSLGVDAQPLPD-CC 32
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W27599 standard; Protein; 601 AA.
W27599;
                                                                                                                                                                                                        18-AUG-1989; US-395773.
(LJOL-) LA JOLLA CANCER RES.
(AMNA-) AMER NAT RED CROSS.
                                                                                                                                                                                                                                                  Ruoslahti EI, Argraves WS;
WPI; 91-087250/12.
N-PSDB; Q11009.
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                                                                                                     .529
                                                                        .484
                                             .479
                                                                                     /label=
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03-APR-1997; U06280.
04-APR-1996; US-627636.
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Bennett LG;
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WO9738014-Al.
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Immediately following each repeat is a pentapeptide with the consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion coplasmic domain of the betal subunit of integrin adhesion ceceptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, aminin, and possibly also other proteins. Antibodies reactive vith the protein have important diagnostic and therapeutic uses. See also R11147, R11149 and R11150.
                                                                                                                                                                                                                                                      Gaps
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180..566
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220..260
/label= repeat unit 2
261..265
/label= conf.
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307..311
//abel= ^~
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/label= repeat unit 6
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144..179
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/label= fibulin B
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R11149 standard; Protein; 601
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ilarity 57.1%;
Conservative
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21-MAY-1991 (first entry)
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/label= re
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:16:02 1999; MasPar time 8.37 Seconds 588.583 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-10 (1-123) from USO8938548B.pep 899 1 VPWAAVTLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

122810 seqs, 40068593 residues

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 40.175; Variance 83.764; scale 0.480 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	0	Query	% Query Matah Tonath DB	ם כ	£	4	
. : Q: :	acore	Maccii	rengen.	9 :	117	Describution	Fred. NO.
Н	106	11.8	619	7	C71413	hypothetical protein	1.65e-02
7	101	11.2	131	1	SEPG	secretin precursor -	7.73e-02
m	96	10.9	641	7	A45054	probable intercellula	1.91e-01
4	96	10.7	601	7	B36346	fibulin 1 precursor,	3.46e-01
Ŋ	96	10.7	683	7	C36346	fibulin 1 precursor,	3.46e-01
9	92	10.2	838	7	145557	eyeless, long form -	1.11e+00
7	91	10.1	440	~	XXHUN	phosphatidylcholine	1.48e+00
80	91	10.1	602	7	S39782	cyclooxygenase 1 - ra	1.48e+00
σ	88	6.6	602	7	S69198	prostaglandin G/H syn	2.61e+00
10	88	ο. ο.	1061	1	OYHUAR	natriuretic peptide r	2.61e+00
11	6 8	6.6	1321	~	T00382	hypothetical protein	2.61e+00
12	88	8.6	226	7	A70565	probable cutinase pre	3.46e+00
13	88	8.6	245	N	S43293	FLT3/FLK2 ligand (clo	3.46e+00
14	88	9.8	254	7	I38427	4-1BB ligand - human	3:46e+00
15	88	8.6	438	Н	XXMSN	phosphatidylcholine	3.46e+00
16	88	8.6	491	~	JC6197	stromelysin 3 (EC 3.4	3.46e+00
17	87	9.7	252	7	B70602	hypothetical protein	4.57e+00
18	87	9.7	583	7	I50518	DNA binding protein E	4.57e+00
19	87	9.7	599	7	A36746	prostaglandin-endoper	4.57e+00
20	86	9.6	322	7	G64151	hypothetical protein	6.03e+00
21	86	9.6	410	7	S74705	hypothetical protein	6.03e+00
22	86	9.6	440	~	JC1502	phosphatidylcholine	6.03e+00
23	86	9.6	497	7	S43745	phosphatidylinositol-	6.03e+00

5 236 2 A37930 placental lactogen pr 7.93e+00 5 236 2 A37930 principal lactogen pr 7.93e+00 5 317 2 S28225 triacylglycerol lipas 7.93e+00 5 317 2 S57275 triacylglycerol lipas 7.93e+00 5 317 2 S28774 centerobactin t 7.93e+00 6 1027 2 S28774 collagen alpha chain 7.93e+00 9 1 ZEBFF4 gene E protein - phag 1.04e+01 9 1 250455 gene E protein - phag 1.04e+01 102 2 S26409 protein - phage 1.04e+01 102 2 S26409 protein 108 precursor 1.04e+01 253 1 C1HUQB protein - phage 1.04e+01 1253 1 C1HUQB protein - phage 1.04e+01 1253 1 C1HUQB protein subcompone 1.04e+01 1315 2 S1434 lutropin-choriogonado 1.04e+01 110topin-choriogonado	ALIGNMENTS  C71413 #type complete hypothetical protein - Arabidopsis thaliana fformal_name Arabidopsis thaliana #common_name mouse-ear cress columbla 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998 C71413 A71403 A71403 A71403 A71403 A71404 A
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. 45000000000000000000000000000000000000	RESULT ENTE ORGANISM #variety DATE ACCESSIONS REFERENCE #authors #journal #title #cross-referent #accession ##status ##residues ##residues ##residues ##residues ##residues ##residues ##arcos-ref GENETICS ##arcos-ref ##residues ##residues ##arcos-ref GENETICS ##arcos-ref ##residues ##arcos-ref ##residues ##arcos-ref ##arcos-re

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##cross-references FlyBase:FBgn0005558

atrons 37/1; 92/2; 152/3; 31/1; 429/1; 521/1; 639/2

atrons #superfamily unassigned homeobox proteins; homeobox homology;

paired box homology

abjernative splicing; DNA binding; homeobox; nucleus;
                                                                                                                                                                                                                                                                                                                                                              Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E. Cell (1989) 58:623-629
Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A34584
Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science (1994) 265:785-789
Homology of the eyeless gene of Drosophila to the Small eye
gene in mice and Aniridia in humans [see comments].
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                                                                                   #authors Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
#journal J. Cell Biol. (1990) 111:3155-3164
#title Fibulin is an extracellular matrix and plasma glycoprotein
with repeated domain structure.
#cross-references MUID:91100426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain signal sequence #status predicted #label SIG\
#product fibulin 1 splice form C #status predicted
#label MAT\
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predicted
#length 683 #molecular-weight 74475 #checksum 7443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eyeless, long form - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
09 Mar-1996 #sequence_revision 09-Mar-1996 #text_change
19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 10-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:X79493; NID:g641809; PID:g641810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 96; DB 2; Lengua v.v., Pred. No. 3.46e-01; V. matches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type protein 30-35,'SX',38-40,'SH',43-44 ##label AR3
                                                                                                                                                                                     #accession C36346
##molecule_type mRNA
##residues 1.683 ##label ARG
##cross-references GB:X53743; NID:g31418; PID:g31419
                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues 1-566 ##label AR2
##cross-references GB:X53741; NID:g31414; PID:g31415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##Erross-references GDB: 778285; OMIM:135820
#map_position 22q13.3-22q13.3
KEYWORDS alternative splicing; glycoprotein
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Best Local Similarity 57.1%;
Matches 16; Conservative
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Rogne, S.; Skretting, G.; Larsen, F.; Myklebost, O.; Mevag, B.; Carlson, L.A.; Holmquist, L.; Gjone, E.; Prydz, H. Biochem. Biophys. Res. Commun. (1987) 148:161-169
The isolation and characterisation of a cDNA clone for human lecithin:cholesterol acyl transferase and its use to analyse the genes in patients with LCAT deficiency and fish
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#title The isolation and characterisation of cDNA and genomic clones
for human lecithin:cholesterol acyltransferase.
#cross-references WUID:88050946
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Waterfield, M.D.; McIntyre, N.; Williamson, R.; Humphries,
                                                                                                                                                                                                                                                                                                                                                                                                          XXHUN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors McLean, J.; Wion, K.; Drayna, D.; Fielding, C.; Lawn, R. #journal Nucleic Acids Res. (1986) 14:9397-9406 #Litle Human lecithin-cholesterol acyltransferase gene: complete gene sequence and sites of expression. #cross-references MulD:87091568 #accession A25575
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lecithin--cholesterol acyltransferase precursor;
phospholipid--cholesterol acyltransferase precursor
                                                          392
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#domain paired box homology #label PBH\
#domain homeobox homology #label HOX
#length 838 #molecular-weight 87662 #checksum
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                                                                                                            Score 92; DB 2; Length 838;
Pred. No. 1.11e+00;
19; Mismatches 17; Indels
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##cross-references GB:M12625; NID:g187022; PID:g307117
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##cross-references GB:X04981; NID:g34286; PID:g34287
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#accession A29661
                                                                                                               Query Match 10.2%;
Best Local Similarity 28.3%;
Matches 15; Conservative
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##residues 13-44
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Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. (1998) 5:169-176
Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.
                                                                                                                                                                                                                                                                            ##cross-references EMBL:AB014534; NID:d1204289; PID:d1032570
                                                                                                                                                                                                        preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                               ##experimental_source brain
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##residues 1-13
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       atrial natriuretic peptide receptor a trionatriuretic peptide receptor A: guanylate cyclase A, membrane-bound guanylate cyclase (EC 4.6.1.2) A #formal_name Homo sapiens #common_name man 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Pardhasaradhi, K.; Kutty, R.K.; Gentleman, S.; Krishna, G. #journal Cell. Mol. Neurobiol. (1994) 14:1-7
#title Expression of mRNA for atrial natriuretic peptide receptor guanylate cyclase (ANPRA) in human retina.
#cross-references MulD:95042574
#accession 152846
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#domain natriuretic peptide-binding domain homology
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#formal_name Homo sapiens #common_name man
01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
                                                                                                                                                                                                 Lowe, D.G.; Chang, M.S.; Hellmiss, R.; Chen, E.; Singh, Garbers, D.L.; Goeddel, D.V.
EMBO J. (1989) 8:1377-1384
                                                                                                                                                                                                                                                              #title Human atrial natriuretic peptide receptor defines a new paradigm for second messenger signal transduction. #cross-references MUID:89356605
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natriuretic peptide receptor A precursor - human
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##molecule_type mRNA
##residues 634-1048 ##label RES
##cross-references GB:S72628; NID:g619241
##experimental_source retina
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##cross-references EMBL:X15357; NID:g28229; PID:g28230
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##cross-references GDB:125199; OMIM:108960
#map_position 1q21-1q22
CLASSIFICATION #sunamf----
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                                                                                                                DATE
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#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III. C.E.; Tekaia, F.; Badcock, R.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, R.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLen, J.; Moule, S.; Murphy, L.; Ollver, S.; Osborne, J.; Quail, M.A.; Safelon, S.; Squres, R.; Sulston, J.E.; Skelton, S.; Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Taylor, K.; Whitehead, S.; Barrell, B.G. Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
                                                                   ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-226 ##label COL
##cross-references GB:295390; GB:AL123456; NID:g3261766; PID:e316057;
PID:g2104375
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                                                                                                                                                                                                                                                                                  A70565 #type complete
probable cutinase precursor - Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                 (strain H37RV)

#formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                      Gaps
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                                                                   3
        Length 1321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 226 #molecular-weight 23113
     Score 89; DB 2; L
Pred. No. 2.61e+00;
5; Mismatches 7,
                                                                                                                  69 LLFLLLLPPPPLLAGATAAASREPDSPCRLKT 100
                                                                                                                                              translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##experimental_source strain H37Rv
                                    Pred.
Query Match
Best Local Similarity 53.18;
Matches 17; Conservative
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protein - protein database search, using Smith-Waterman algorithm Fri Aug 20 21:18:21 1999; MasPar time 2.85 Seconds 437.587 Million cell updates/sec MPsrch\_pp

Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-938-548B-10 (1-123) from US08938548B.pep 899 1 VPWAAVTLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123

PAM 150 Gap 11 Scoring table:

Searched:

Post-processing:

106580 seqs, 10152877 residues

Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 27.574; Variance 124.910; scale 0.221

Statistics:

SUMMARIES

	Pred. No.	9.49e+00	1.32e+01	2.57e+01	2.57e+01	2.57e+01	2.57e+01	3.02e+01	3.02e+01	3.02e+01	3.02e+01	3.56e+01	3.56e+01	4.18e+01	4.18e+01	4.18e+01	4.18e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	5.78e+01	5.78e+01	5.78e+01
		Applicatio	Applicatio	Applicatio	5175255.	Applicatio	498600.	5175255.	5175255.	Applicatio	Applicatio	Applicatio	Applicati	Applicatio	Applicatio	5194596.	Applicatio							
	Description	Sequence 3,	Sequence 4,	Sequence 5,	Sequence 2,	Sequence 2,	Sequence 3,	Sequence 6,	Sequence 6,		ď	ċ	Sequence 4,	Patent No. 5	Patent No. 5	Patent No. 5	Sequence 1,		Sednence 4,	Sequence 12,	'n	Sequence 4,	Patent No. 5	Sequence 9,
SUMMARIES	ID	US-08-749-	US-08-236-	US-08-299-	US-08-453-	US-08-240-	US-08-026-	US-08-993-	US-08-243-	PCT-US94-0	PCT-US91-0	5175255-4	US-08-804-	5498600-2	5175255-8	5175255-2	US-08-445-	US-08-001-	US-07-794-	US-08-555-	PCT-US95-0	US-08-387-	5194596-15	PCT-US96-0
	DB	- 2	٦	Н	Н	Ч	Н	7	Н	٣	٣	4	7	4	4	4	Н	Н		~	m	Н	4	r
	Query Match Length	954	254	234	238	238	1239	235	235	235	263	220	3729	226	241	241	282	492	492	684	1337	241	241	241
de	Query Match	10.0	8.6	9.3	9.3	6.6	9.3	9.5	9.5	9.2	9.5	9.1	9.1	0.6	9.0	0.6		8.9	ø. 9	8.9	٠.		8.8	8.8
	Score	06	88	84	84	84	84	83	83	83	83	82	82	81	81	81	81	80	80	80	80	79	79	79
	Result No.		7	m	4	5	9	7	∞	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

5.73 6.7386			
Sequence 5, Application Sequence 8, Application Sequence 1, Application Sequence 20, Application Sequence 20, Application Sequence 20, Application Sequence 20, Application Sequence 3, Application Sequence 3, Application Sequence 2, Application Sequence 3, Application Se	954 AA.	IONS #1.25	
US-08-693- Se US-08-693- Se US-08-693- Se US-08-693- Se US-08-693- Se US-08-484- Se US-08-68-65- Se US-08-68-65- Se US-08-68-65- Se US-08-68-1 Se US-08-65- Se US	ALIGNMENTS STANDARD; PRT;	A POSIT 0.0, V 169A 7,169A	In MW; 4424673 CN;
8 3170 442 2 445 2 7.7 442 2 7.7 1184 1 7.7 1184 2 7.7 1184 1 7.7 1184 1 7.7 1184 1 7.7 1184 2 7.7 1187 1 7.8 1187 1 7.8 1187 1 7.9 1187 1 7.0 1187 2 7.0 1187	۳	Peplication Under State of Sta	ire: procein 34 AA; 101960 MW;
777777777777777777777777777777777777777	T US-08-749-169A XXXXXX	Sequence 3, Application US/087491699 Sequence 3, Application US/087491699 Patent No. 5846770 GENERAL INFORMATION: APPLICANT: EAVALLIE, EGWARD APPLICANT: LORDALLIE, EGWARD TITLE OF INVENTION: CHORDIN COM NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: Genetics Institute STREET: 87 CambridgePark Driv. CITY: Cambridge STATE: MASSACHUSELTS TOP: 02140 COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BATCHIN BRIES ATTORNEY AGENT INFORMATION: APPLICATION NUMBER: US/08/749 FILING DATE: CLASSIFICATION NUMBER: US/08/749 FILEPAX: (617) 498-8260 TELEFAX: (617) 498-8260 TELEFAX: (617) 498-8261	SEQUENCE 954
90000000000000000000000000000000000000	SUL	% % # # # # # # # # # # # # # # # # # #	

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Gaps
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Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishiohata Residence 1-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                                                                                                             COMPUTER FEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1239 AA
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STREET: 5214, Mishionata-machi
CITY: Nilgata-shi
STATE: Nilgata-ken
COUNTRY: JAPAN
ZIP: 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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JENCE 238 AA; 26350 MW; 315668 CN;
           ADDRESSE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08026138E
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amino acid
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                                                                                                                                                          COUNTRY:
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Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETIT, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SOUDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84; DB 1; Length 238; Pred. No. 2.57e+01; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintoon
COMPUTER: Apple Macintoon
COPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30 MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
APPLICATION NUMBER: US 08/161,132
FILING DATE: 09-MAY-1994
APPLICATION DATA:
APPLICATION UNBER: US 08/114,426
FILING DATE: 20-Aug-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION UNBER: 32,172
REFERENCE/DOCKET NUMBER: 33,172
REFERENCE/DOCKET NUMBER: 31,172
REFERENCE/DOCKET NUMBER: 31,172
REFERENCE/DOCKET NUMBER: 33,172
REFERENCE/DOCKET NUMBER: 32,172
REGISTER NUMBER: 32,172
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MOLECULE TYPE: protein
FENCE 238 AA; 26350 MW; 315668 CN;
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                                                                                                                                           ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
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Best Local Similarity 68.4%;
Matches 13; Conservative
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Sequence 2, Application PC/TUS9106532
GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Vaccines and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two First National Plaza Suite 2100
CITY: Chicago
STATE: Illinois
ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 235 amino acids
amino acid
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2 PWAAVT-LLLLLLEPPAL 18
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PCT-US91-06532-2
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for fll3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.2%; Score 83; DB 1; Length 235; Best Local Similarity 55.6%; Pred. No. 3.02e+01; Matches 10; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
COMPRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAX-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: AUGUST 25, 1993
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 537-0430
TELEPHONE: (206) 233-0644
TELEX: 7568-2
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
CLASSIFICATION: 435
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MOLECULE TYPE: protein
JENCE 235 AA; 26415 MW; 293990 CN;
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2 PWAAVT-LLLLLLLPPAL 18
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9.2%; Score 83; DB 3; Length 235;
Best Local Similarity 55.6%; Pred. No. 3.02e+01;
Matches 10; Conservative 6; Mismatches 1; Indels
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: -to be assigned-FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: AUGUST 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: AUGUST 12, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 28,1993
CLASSIFICATION NUMBER: 28,555
FILING DATE: May 24, 1993
CLASSIFICATION NUMBER: 28,555
REGISTRATION NUMBER: 28,655
REFERENCE/ODCKET NUMBER: 28,655
REFERENCE/ODC
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JENCE 235 AA; 26415 MW; 293990 CN;
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomason, Arlen R.; Nicholson, Margery
TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                     Length 226;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
SEQ ID NO:2:
                                                                                                                                                                                                                                                                             245 AA; 27563 MW; 324570 CN;
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4CE 261 AA; 29326 MW; 367179 CN;
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APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986
PPLICATION NUMBER: 896,485
FILING DATE: 3-AUG-1986
APPLICATION NUMBER: 705,175
FILING DATE: 25-FEB-1985
APPLICATION NUMBER: 660,496
FILING DATE: 12-OCT-1984
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Page 1

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Aug 20 21:16:51 1999; MasPar time 5.77 Seconds 602.480 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-10 (1-123) from US08938548B.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

77977 segs, 28268293 residues

Searched:

swiss-prot37 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.468; Variance 75.472; scale 0.549

### SUMMARIES

		dР			Continue		
Result No.	Score	Query	Length	DB	ID	Description	Pred. No.
↔	103	11.5	567	Н	GPV_RAT	PLATELET GLYCOPROTEIN	8.73e-03
~	101	11.2	131	Н	SECR_PIG	SECRETIN PRECURSOR (FR	1.73e-02
m	96	10.7	566	Н	FBLA_HUMAN	FIBULIN-1, ISOFORM A P	9.21e-02
4	96	10.7	601	Н	FBLB_HUMAN	FIBULIN-1, ISOFORM B P	9.21e-02
Ŋ	96	10.7	683	Н	FBLC_HUMAN	FIBULIN-1, ISOFORM C P	9.21e-02
9	96	10.7	703	<del></del> 1	FBLD_HUMAN	FIBULIN-1, ISOFORM D P	9.21e-02
7	91	10.1	440	Н	LCAT_HUMAN	PHOSPHATIDYLCHOLINE-ST	4.64e-01
ω	88	9.9	602	-	PGH1_RAT	PROSTAGLANDIN G/H SYNT	8.72e-01
σ	88	9.9	1001	~	ANPA_HUMAN	ATRIAL NATRIURETIC PEP	8.72e-01
10	88	9.8	254	٦	41BL_HUMAN	4-1BB LIGAND (4-1BBL).	1.19e+00
11	88	9.8	438	H	LCAT_MOUSE	PHOSPHATIDYLCHOLINE-ST	1.19e+00
12	98	•	322	Н	RLUC_HAEIN	RIBOSOMAL LARGE SUBUNI	2.20e+00
13	86		440	Н	LCAT_PAPAN	PHOSPHATIDYLCHOLINE-ST	2.20e+00
14	98	•	497	г	SC14_YARLI	SEC14 CYTOSOLIC FACTOR	2.20e+00
15	98	9.6	1663	7	CO3_RAT	COMPLEMENT C3 PRECURSO	2.20e+00
16	85	9.5	236	П	PLC1_BOVIN	PLACENTAL LACTOGEN I P	2.98e+00
17	82	9.5	317	П	LIP1_PSYIM	LIPASE 1 PRECURSOR (EC	2.98e+00
18	85	9.5	334	П	FEPD_ECOLI	FERRIC ENTEROBACTIN TR	2.98e+00
19	82	9.5	1027	П	CAFF_RIFPA	FIBRIL-FORMING COLLAGE	2.98e+00
20	84	9.3	90	П	VGE_BPPHX	LYSIS PROTEIN (E PROTE	4.03e+00
21	84	9.3	06	Н	VGE_BPS13	LYSIS PROTEIN (E PROTE	4.03e+00
22	84	9.3	238	Н	EFA3_HUMAN	EPHRIN-A3 PRECURSOR (E	4.03e+00
23	84	9.3	251	П	C1QB_HUMAN	COMPLEMENT C10 SUBCOMP	4.03e+00

4 4 4 4 4 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0
LIPASE 3 PRECURSOR (ECRIBOSOMAL LARGE SUBUNI GTPASE ACTIVATING PROTIUTROPIN-TROBING PROTEIN-TROBINE PROSENTALIN.  PLATELET GINCOPROTEIN OXALATE OXIDASE PRECURSOR INFECTED CELL PROTEIN TROSPHATIDYLCHOLINE-ST PHOSPHATIDYLCHOLINE-ST PHOSPHATIDYLCHOLINE-ST PHOSPHATIDYLCHOLINE-ST PHOSPHATION PROTEIN TRANS-ACTING TRANSCRIP PROTEIN TRANS-ACTING TRANSCRIP PROTEIN TRANS-ACTING TRANSCRIP PROTEIN-TYROSINE PHOSP RETINAL GUANTIAL CUCLAR ANGIOTENSIN-CONVERTING
LIP3_MORSP RLUC_ECOLI ISN_DROME ISN_DROME ISN_DROME TALI_MOUSE GPBB_PAPCY OXO2_HORVU ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP3_HSV11 ICP0_HSV8V1 PTEN_ECOLI ALBU_CHICK AL
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### ALIGNMENTS

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ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.; "Fibulin is an extracellular matrix and plasma glycoprotein with
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MEDLINE: 89354537.
ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHII E.;
ARGRAVES W. an owel protein that interacts with the fibronectin receptor beta subunit cytoplasmic domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , DB 1; Lengt.
, 9.21e-02;
... 8; Indels
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A2D23E14 CRC32;
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01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM B PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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Pred. No.
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CELL BIOL. 111:3155-3164(1990).
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Best Local Similarity 57.1%;
Matches 16; Conservative
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566 AA;
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REPEAT; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
"Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.";
                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 1,
EGF-LIKE 1,
EGF-LIKE 2,
CALCIUM-BINDING
EGF-LIKE 5,
CALCIUM-BINDING
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                                                        FBLA_HUMAN STANDARD; PRT; 566 AA. p23142; 500 AA. p23142; 500 AA. p13142; 500 AA. p13142; 500 LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
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PROSITE: PS00022; EGF_1; FALSE_NEG.
PROSITE: PS01177; ANAPHYLATOXIN_1; 3.
PROSITE: PS01178; ANAPHYLATOXIN_2; 3.
PROSITE: PS01186; EGF_2; 3.
PROSITE: PS01186; EGF_2; 3.
PROSITE: PS01086; EGF_2; 5.
HSSP; P35555; 1EMO.
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TLLLLLLLPPALLSLGVDAQPLP 29
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                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
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FIBULIN-1, ISOFORM C.

ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIK
PROSITE; PS01187; EGF_CA; 8.
PFAM: PF00008; EGF; 5.
HSSP; P3555; 1EMO.
SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX;
REPEAT; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.
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Best Local Similarity 57.1%;
Matches 16; Conservative
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SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (SEP-1993) TO EMBL/GENBANK MATRIX.
SUBGELLGUAR LOCATION: EXTRACELLULAR MATRIX.
CALPARATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (AC P23142), B (AC P23143), C (AC P23144) AND D (SHOWN HERE); DIFFERING ONLY IT THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; REPEAT; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
                             01-OCT-1994 (REL. 30, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM D PRECURSOR.
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MIM; 135820; -.
PROSITE; PS00010; ASX HYDROXYL; 4.
PROSITE; PS00010; ASX HYDROXYL; 4.
PROSITE; PS01017; ANAPHYLATOXIN_1; 3.
PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 8.
PRAM; PRO0008; EGF, 5.
HSSP; P35555; 1EMO.
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Gaps

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8; Indels

10 VPLPLLLGGLALLAAGVDADVLLEACC 37

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g ò RESULT

US-08-938-548B-10.rsp

JQ0036; JQ0036.

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CATALITIC ACTIVITY: PHOSPHATICHOLINE + STEROL = STEROL ESTER + 1-ACYLGIVCEROPHOSPHOCHOLINE (PALMITOLL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERRED: A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Deficiency of lecithin: cholesterol acyltransferase due to compound heterozygosity of two novel mutations (Gly33Arg and 30 bp ins) in the
                                                                                                                                                                        "Genetic and phenotypic heterogeneity in familial lecithin:
cholesterol acyltransferase (LCAT) deficiency. Six newly identified
defective alleles further contribute to the structural heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A single G to A nucleotide transition in exon IV of the lecithin: cholesterol acyltransferase (LCAT) gene results in an Arg140 to His substitution and causes LCAT-deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNKE H., ASSMANN G.; "Complete deficiency of plasma lecithin-cholesterol acyltransferase (LCAI) activity due to a novel homozygous mutation (Gly-30-Ser) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HILL J.S., O K., WANG X., PRITCHARD P.H.; "Lecithin:cholesterol acyltransferase deficiency: identification of causative gene mutation and a co-inherited protein polymorphism."; BIOCHIM. BIOPHYS. ACTA 1181:321-323(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT HIS-164.
BEDILNE: 95331753.
STETRER E.: HAUBENWALLNER S., HOERL G., GIESSAUF W., KOSTNER G.M.,
ZECHNER R.;
FUNKE H., VON ECKARDSTEIN A., PRITCHARD P.H., HORNBY A.E., WIEBUSCH H., MOTTI C., HAYDEN M.R., DACHET C., JACOTOT B., GERDES FAERGEMAN O., ALBERS J.J., COLLEONI N., CATAPANO A., FROHLICH J., ASSMANN G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95227171.
WIEBUSCH H., CULLEN P., OWEN J.S., COLLINS D., SHARP P.S., FUNKE
ASSMANN G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIS ENZYME.
DISEASE: DEFECTS IN LCAT ARE THE CAUSE OF NORUM AND FISH EYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96400966.
OWEN J.S., WIEBUSCH H., CULLEN P., WATTS G.F., LIMA V.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS. ARG-57 AND 10 AA INSERTION IN POSITION 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ымы, XU6537; -; NOT ANNOTATED_CDS.
EMBL, M26268; G187025; -.
EMBL, X04981; G34287; -.
EMBL, M17959; G366858; -.
                                                                                                                                                                                                                                                                                           in this disease.";
J. CLIN. INVEST. 91:677-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.";
MOL. GENET. 4:143-145(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENET. 96:105-109(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS THR-117 AND CYS-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUM. MUTAT. 8:79-82(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M12625; G307117; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT AS ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93305754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT SER-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCAT gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME
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A25575; A25575 PIR; A00571; XXHUN. PIR; A29661; A29661 PIR; A25575; A25575

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                                                                                                                                                                                                                                                                                                                                                                             PGH1_RAT STANDARD; PRT; 602 AA.

063921; Q62731; Q63684;

15-DEC-1998 (REL. 37, CREATED)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN H2

SYNTHASE 1) (PGH SYNTHASE 1) (PGHS-1) (PHS 1).

PTGS1 OR COX1 OR COX-1.

RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
THIS ENZYME ACTS BOTH AS DOUNCENASE AND AS A PEROXIDASE.
THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) = PROSTAGLANDIN
                                     PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E., WILSON C.B., HWANG D., "Cloning two isoforms of rat cyclooxygenase: differential regulation of their expression.";
                                                                                                                                                                                                                                                                      Gaps
                                                                                              LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H2 + A + H(2)O.
-!- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                      Score 91; DB 1; Length 440;
Pred. No. 4.64e-01;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARCH. BIOCHEM. BIOPHYS. 307:361-368(1993)
                                                                                                                                                                                                               omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FISHER 344; TISSUE-TRACHEA; MEDLINE; 95168876.
                                                                     DISEASE MUTATION.
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.3%;
Matches 13; Conservative
                                                                                                                                                                                                            of annotations
                                                                                                                                                                                                                                                                                               7 PWQWVTLLLGLLLPPA 22
                                                                                                                                                                                                                                                                                                             440
205
98
380
                                                                                                                                                     44
108
296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRAGUE-DAWLEY; MEDLINE; 94099619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUCH AS ASPIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THROMBOXANES
                                                                                               25
205
74
337
                                                                     POLYMORPHISM;
                           MIM; 245900
                                                                                                                                                                                                     Note: remainder
                                                                                                            ACT_SITE
DISULFID
                                                                                                                                      DISULFID
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                     CARBOHYD
                                                                                 SIGNAL
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C68C1B27 CRC32;

26624 MW;

254 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                              EUR. J. IMMUNOL. 24:2219-2227(1994).

-!- FUNCTION: INDUCES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD

T CELLS. MAY HAVE A ROLE IN ACTIVATION-INDUCED CELL DEATH (AICD).

MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN T CELLS AND

B CELLS/MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94374434.
ALDERSON M.R., SMITH C.A., TOUGH T.W., DAVIS-SMITH T., ARMITAGE R.J., FALK B., FOUX E., BAKER E., SUTHERLAND G.R., DIN W.S., GOODWIN R.G.; "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B CELLS/MACROPHAGES.
SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLUIAR LOCATION: TYPE II MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
                                                                                                                                                                                                   Gaps
        NATRIURETIC PEPTIDE RECEPTOR A.
                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                              Score 89; DB 1; Length 1061;
Pred. No. 8.72e-01;
0; Mismatches 6; Indels
              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEIN; SIGNAL-ANCHOR.
                                     CYTOPLASMIC (POTENTIAL)
                                                                        INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
POTENTIAL.
                                            PROTEIN KINASE LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                             C6117B45 CRC32;
                                                                                                                                                                                                                                                                        41BL_HUMAN STANDARD; PRT; 254 AM. P41273; 01-FEB-1995 (REL. 31, CREATED) 01-FEB-1996 (REL. 31, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) 4-1BBL LICAND (4-1BBL).
                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                               9.98;
                                                                                                                                                                                      68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U03398; G571323; -.
                                                                                                                                                                                                  Conservative
32
1061
473
473
1061
805
1118
2455
455
34
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49
254
41
                                                                                                    45
212
338
379
386
                                                                                                                                                    427 43
1061 AA;
                                                                                                                                                                                       Local Similarity
les 15; Conser
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 94374434.
      DOMAIN
DOMAIN
DISULFID
                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                         CARBOHYD
CARBOHYD
                 DOMAIN
TRANSMEM
                                                              DISULFID
                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                       ligand.";
                                                                                                                                                            SEQUENCE
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERONI G., MALGARETTI N., MAGNAGHI P., TARAMELLI R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
ILPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTERD. TRANSPORTEINS IT ENTERNIETS THE FREE CHOLESTERD TRANSPORTEINS.
ILPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTERY FALSOME STANDSTRATE ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL ESTER + 1-ACYLGIXCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERED; A NUMBER OF STEROLS, INCLUDING CHOLESTERD, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin: cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver."; J. BIOL. CHEM. 264:21573-21581(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A3418; XXMSN.
MGD; MGI:9675; LCAT.
PROSITE; PS00120; LIPASE_SER; 1.
PROSITE; PS0120; LIPASE_SER; 1.
SIGNAL.
1 24
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT AS ACCEPTOR). ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIS ENZYME.
-:- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                                                                                                                                    01-AGG-1990 (REL. 15, CREATED)
01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-AGV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90094326.
WARDEN C.H., LANGNER C.A., GORDON J.I., TAYLOR B.A., MCLEAN J.W.,
                                                               ή;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
Score 88; DB 1; Length 254;
Pred. No. 1.19e+00;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                      438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                      PRT;
   Query Match 9.8%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                      27 LPWALVAGLLLLLLLAAA 44
                                                                                                                                                       1 VPWAAVT-LLLLLLPPA 17
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EMBL; X54095; G52874; -.
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                                                                                                                                                                                                                                                                                             LCAT_MOUSE P16301;
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SUNDSTROM S.A., KOMM B.S., PONCE-DE-LEON H., YI Z., TEUSCHER C.,
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                           LYTTLE C.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                      SEQUENCE FROM N.A.

C STRAIN-ATCZ 20460 / W29;

MEDLINE; 9418653:

A LOPEZ M.C., NICAUD J.-M., SKINNER H.B., VERGNOLLE C., KADER J.-C.,

A BANKAITIS V., GAILLARDIN C.;

"A phosphatidylinositol/phosphatidylcholine transfer protein is

required for differentiation of the dimorphic yeast Yarrowia

I ipolytica from the yeast to the mycelial form.";

J. CELL BIOL. 124.113.127(1994).

C. II. FUNCTION: REQUIRED FOR TRANSPORT OF SECRETORY PROTEINS FROM THE

GOLGI COMPLEX. CATALYZES THE TRANSFER OF PHOSPHATIDYLINOSITOL AND

PHOSPHATIDYLCHOLINE BETWEEN MEMBRANES IN VITRO.

C. II. SUBCELLULAR LOCATION: ASSOCIATED WITH THE GOLGI COMPLEX AS A

PERIPHERAL MEMBRANE PROTEIN (BY SIMILARITY).

C. I. SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
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STRAIN=WISTAR; TISSUE-LIVER;
MEDLINE; 90.245672.
MISUMI Y., SOHDA M., IKEHARA Y.;
"Nucleotide and deduced amino acid sequence of rat complement C3.";
NUCLEIC ACIDS RES. 18:2178-2178(1990).
  FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 79062262.
JACOBS J.W., RUBIN J.S., HUGLI T.E., BOGARDT R.A., MARIZ I.K.,
DANIELS J.S., DAUGHADAY W.H., BRADSHAW R.A.;
"Purification, characterization, and amino acid sequence of ra
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 497;
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01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AVLLLLELLLPSRLLLPRLLLPRRQGSRSRCCQDRHCPC 390
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Pred. No. 2.20e+00;
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LEU-RICH.
6209E8FC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPORT; PROTEIN TRANSPORT; GOLGI STACK.
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BIOCHEMISTRY 17:5031-5038(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1316-1595 FROM N.A.
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Local Similarity 45.0%;
les 18; Conservative
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                     DIPODASCACEAE; YARROWIA
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    EUKARYOTA;
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P01026;
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0
"Estrogen regulation of tissue-specific expression of complement C3."; J. BJOL. CHEM. 264.16947 (1989).
-!- FUNCTION: C3 PLAYS A CENTRAL ROLE. IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
                                                                    COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL AREACTYON IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.

AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SYNEACE CARBOHYDRATES OR IMMUNE AGGREGATES. FUNCTION: DERIVED FROM PROTEOLYTIC DECRADATION OF COMPLEMENT C3, C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDICES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
                                                                                                                                                                                                                                                                                       SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETR 6 ALDHA, LINKED BY A DISULEIDE BOND. C3 CONVERTARE AS BOYD. C3 CONVERTARE C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLATOXIN 6 GENERATING C3B (BETA CHAIN + ALPHA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-i- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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Pred. No. 2.20e+00;
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MW; 0428CF63 CRC32;
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EMBL; M29866; G554423; ALT_SEQ.
PIR; A01260, A01260.
PIR; S15764; S15764.
PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
PRAM: PF00207; A24; 1.
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Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

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>US-08-938-548B-10 (1-123) from US08938548B.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_bhage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 39.662; Variance 86.129; scale 0.460 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

6.00e-145	3.85e-136,	1.82e-113	2.23e-111	3.75e-03	3.22e-02	3.44e-01	6.13e-01	1.08e+00	1.44e + 00	1.44e + 00	1.90e+00	1.90e+00	3.32e+00	3.32e+00	4.36e+00	5.73e+00	5.73e+00	7.52e+00	7.52e+00
HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	GDNF FAMILY RECEPTOR A	HYPOTHETICAL 74.6 KD P	FRIZZLED PROTEIN HOMOL	FRIZZLED-1.	ACYLOXYACYL HYDROLASE.	LEUCINE ZIPPER WITH BA	TIGHT JUNCTION PROTEIN	PROLINE- AND LEUCINE-R	PAIRED BOX PROTEIN PAX	L-1 METALLO-BETA-LACTA	SORTILIN PRECURSOR.	KIAA0634 PROTEIN (FRAG	HYPOTHETICAL 23.1 KD P	THYROID HORMONE INDUCE	HYPOTHETICAL 25.9 KD P	PUTATIVE GPI-ANCHORED
055241	055232	043612	077668	609090	023352	008463	070421	035298	091640	095168	041051	018381	051899	099523	075129	006319	091654	005582	02660
11	11	4	9	4	10	Π	H	디	13	ø	10	Ŋ	7	4	4	7	13	7	ß
130	130	131	131	400	619	641	626	574	331	1174	106	857	290	833	1321	226	335	252	396
100.0	94.9	81.6	80.4	12.6	11.8	10.9	10.7	10.5	10.3	10.3	10.2	10.2	10.0	10.0	6.6	9.6	9.8	9.7	9.7
899	853	734	723	113	106	86	96	94	93	6	92	92	06	06	89	88	88	87	87
н	7	3	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20
	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 81.6 131 4 043612 PREPRO-OREXIN. 1.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6.94.9 130 11 055232 PREPRO-OREXIN. 3.81.6 131 4 077668 PREPRO-OREXIN PRECURSO 2.100.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 81.6 131 4 043612 PREPRO-OREXIN. 1. 80.4 131 6 077668 PREPRO-OREXIN PRECURSO 2. 12.6 400 4 060609 GDNF FAMILY RECEPTOR A 3.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 81.6 131 4 043612 PREPRO-OREXIN. 80.4 131 6 077668 PREPRO-OREXIN PRECURSO 2. 12.6 400 4 060609 GDNF FAMILY RECEPTOR 8. 3. 11.8 679 10 023352 HYPOTHETICAL 74.6 KD P. 3.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 98.4 131 4 043512 PREPRO-OREXIN. 13.1 6 077668 PREPRO-OREXIN PRECURSO 2. 12.6 400 4 060609 GDNF FAMILY RECEPTOR A 3. 11.8 679 10 023352 HYPOTHETICAL 74.6 KD P 3. 10.9 641 11 008463 FRIZZLED PROPENH HOMOL 3.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6.94.9 130 11 055232 PREPRO-OREXIN. 3.981.6 131 4 074612 PREPRO-OREXIN. 1.080.4 131 6 077668 PREPRO-OREXIN PRECURSO 2.12.6 400 4 060609 GDNF FAMILY RECEPTOR A 3.11.8 679 10 023352 HYPOTHETICAL 74.6 KD P 3.10.7 641 11 008463 FRIZZLED PROTEIN HOMOL 3.10.7 626 11 070421 FRIZZLED-1. 6.13	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6.94.9 130 11 055232 PREPRO-OREXIN. 3.1 4 043612 PREPRO-OREXIN. 1.0 12.6 400 4 060609 GDNF FAMILY PRECEPTOR 7.1 11.8 679 10 023352 HYPOTHETICAL 74.6 KD P. 3.1 679 10 023352 HYPOTHETICAL 74.6 KD P. 3.1 10.9 641 11 008463 FRIZZLED-17.6 KD P. 3.1 10.5 574 11 035298 AYLOXPACYL HYDROLASE. 1.1	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 94.9 130 11 055232 PREPRO-OREXIN. 3. 90.4 131 6 077668 PREPRO-OREXIN. 12.6 400 4 060609 GDNF FAMILY RECEPTOR A 3. 11.8 679 10 03552 HYPOTHETICAL 74.6 KD P 3. 10.9 641 11 008463 FRIZZLED PROFIN HOMOL 3. 10.7 626 11 070421 FRIZZLED PROFIN HOMOL 5. 574 11 035298 ACYLOXYACYL HYDROLASE. 10.3 331 13 099640 LEUCINE ZIPPER WITH BA 1.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 91.6 131 4 073612 PREPRO-OREXIN. 1. 91.4 6 077668 PREPRO-OREXIN. 1. 91.6 470 4 060609 GDNF FAMILY RECEPTOR A 3. 11.8 679 10 023352 HYPOTHETICAL 74.6 KD P. 3. 10.9 641 11 008463 FRIZZLED PROTEIN HOMOL 3. 10.7 626 11 070421 FRIZZLED-1. 6. 6. 10.7 626 11 070421 PRIZZLED-1. 6. 10.5 574 11 035298 ACYLOXYRACYL HYDROLASE. 1. 10.3 331 33 091640 LEUCINE ZIPPER WITH BA 1. 10.3 174 6 099168	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6.94.9 130 11 055232 PREPRO-OREXIN. 3.61.6 131 4 054012 PREPRO-OREXIN. 1.1 4 077668 PREPRO-OREXIN. 1.2 6 400 4 060609 GDNF FAMILY RECEPTOR A 3.1 1.8 679 10 023352 HYPOTHETICAL 74.6 KD P 3.1 10.9 641 11 008463 FRIZZLED PROTEIN HOMOL 3.1 10.5 574 11 055298 ACYLOXYACYL HYDROLASE. 1.1 10.3 331 13 091640 LEGGINE ZIPPER WITH BA 1.1 10.1 106 10 041051 PROLINE AND LEGGINE II.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 91.0 131 4 043612 PREPRO-OREXIN. 1. 91.1 4 043612 PREPRO-OREXIN. 1. 91.6 470 4 060609 GDNF FAMILY RECEPTOR A 3. 11.8 679 10 023352 HYPOTHETICAL 74.6 KD P 3. 10.9 641 11 008463 FRIZZLED PROTEIN HOMOL 3. 10.5 574 11 035298 ACLOXYACYL HYDROLASE. 10.3 331 13 091640 LEUCINE ZIPPER WITH BA 1. 10.3 1174 6 095168 TIGHT JONGTION PROTEIN 1. 10.2 106 041051 PROLINE AND LEUCINE. 1. 10.2 106 041051 PROLINE. 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AND LEUCINE	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 91.6 131 4 073612 PREPRO-OREXIN. 1. 131 4 077668 PREPRO-OREXIN. 1. 131 4 077668 PREPRO-OREXIN. 1. 12.6 400 4 060609 GDNF FAMILY RECEPTOR A 3. 11.9 679 10 023352 HYPOTHETICAL 74.6 KD P. 3. 10.9 641 11 008463 FRIZZLED PROTEIN HOMOL 10.7 626 11 070421 FRIZZLED PROTEIN HOMOL 6. 10.5 574 11 035298 ACYLOXYRACXL HYDROLASE. 11. 3. 31 13 091640 LEUCINE ZIPPER WITH BA. 10.3 1174 6 095168 TIGHT JUNCTION PROTEIN 11. 10.2 106 10 041051 PAIRED BOX PROTEIN PAIRED PAIRED BOX PROTEIN PAIRED BOX PROTEIN PAIRED PAI	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6.94.9 130 11 055232 PREPRO-OREXIN. 3.081.4 043612 PREPRO-OREXIN. 1.081.4 043612 PREPRO-OREXIN. 1.081.4 040 4 060609 GDNF FAMILY RECEPTOR A 3.10.9 641 11 008463 FRIZZLED PROTEIN HOMOL 10.7 626 11 070421 FRIZZLED PROTEIN HOMOL 10.5 574 11 035298 ACYLOXYACYL HYDROLASE. 1.0.3 311 13 091640 LEUCINE ZIPPER WITH BA 1.10.3 331 13 091640 LEUCINE ZIPPER WITH BA 1.10.2 106 10 041051 PROLINE AND LEUCINE. 11.10.2 857 5 018381 PAIRED BOX PROTEIN PAX 1.10.2 857 5 018391 L-1 METALLO-BETA-LACTA 3.10.0 833 4 099523 SORTILIN PRECURSOR. 3.3	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 91.0 130 11 055232 PREPRO-OREXIN. 1.0 131 4 043612 PREPRO-OREXIN. 1.1 6 077668 PREPRO-OREXIN. 1.1 6 070 4 060609 GDNF FAMILY RECEPTOR A 3. 1.0 9 641 11 008463 FRIZZLED PROTEIN HOMOL 3. 1.0 641 11 008463 FRIZZLED-1. FRIZZLED ROTEIN HOMOL 3. 1.0 574 11 035298 ACYLOXYACYL HYDROLASE. 1.0 331 13 091640 LEGGINE ZIPPER WITH BA 1.1 10.3 331 13 091640 LEGGINE ZIPPER WITH BA 1.1 10.2 6095168 TIGHT JUNCTION PROTEIN 1.1 10.2 106 10 041051 PROLINE AND LEGGINE R. 1.1 METALLO-BETA-LACTA 3. 1.0 0290 2 051899 L.1 METALLO-BETA-LACTA 3. 1.0 833 4 095523 SCRTILIN PRECURSOR. 3. 9.9 1321 4 075129 KTAAO634 PROTEIN (FRAG 4.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 91.6 131 4 055232 PREPRO-OREXIN. 131 4 077668 PREPRO-OREXIN. 131 4 077668 PREPRO-OREXIN. 12.6 400 4 060609 GDNF FAMILY RECEPTOR A 3. 10.9 641 11 008346 PRIZZLED PROTEIN HOMO. 10.7 626 11 070421 FRIZZLED PROTEIN HOMO. 10.5 574 11 035298 ACLOXARACKI HYDROLASE. 10.3 31 13 091640 IEDUCINE ZIPPER WITH BA 110.2 857 5 018381 PAIRED BOX PROTEIN 1. 10.2 857 5 018381 PAIRED BOX PROTEIN PAR. 110.0 833 4 099523 SORTILIN PRECURSOR. 3. 10.0 833 4 075129 KIAROGASE. 1. 1 METALLO-BETA-LACTA 3. 10.0 833 4 075129 KIAROGASE. 3. 10.0 833 4 075129 KIAROGASE. 3. 10.0 833 4 075129 HYPOTHETICAL 23.1 KD P 5.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 91.6 131 4 073628 PREPRO-OREXIN. 1.8 131 4 077668 PREPRO-OREXIN. 1.8 679 10 023352 PREPRO-OREXIN PRECURSO 2. 12.6 4.00 4 060609 GDNF FAMILY RECEPTOR A. 3. 10.7 626 11 070421 PRIZZLED PROTEIN HOMOL 3. 10.7 626 11 070421 PRIZZLED PROTEIN HOMOL 10.3 331 13 091640 LEUCINE ZIPPER WITH BA. 1. 10.3 11 3 091640 LEUCINE ZIPPER WITH BA. 1. 10.2 857 5 018381 PROLINE AND LEUCINE-R 1. 10.2 857 5 018381 PROLINE AND LEUCINE-R 1. 10.0 290 2 051899 SORTILIN PRECURSOR. 3. 9.9 1321 4 075129 KIAA0634 PROTEIN PRECURSOR. 3. 9.8 226 2 006319 HYPOTHETICAL 23.1 KD P. 5. 9.8 325 13 094654 HYPOTHETICAL 23.1 KD P. 5. 9.8 325 13 094654 HYPOTHETICAL 23.1 KD P. 5.	100.0 130 11 055241 HYPOCRETIN (PREPRO-ORE 6. 94.9 130 11 055232 PREPRO-OREXIN. 3. 131 4 073612 PREPRO-OREXIN. 1. 131 4 073612 PREPRO-OREXIN. 1. 131 4 073669 GDNF FAMILY RECEPTOR A 3. 11.8 679 10 023352 HYPOTHETICAL 74.6 KD P 3. 10.9 641 11 070421 FRIZZLED PROTEIN HOMOL 3. 10.5 574 11 035298 ACYLOXYACYL HYDOLASE. 11. 10.5 331 13 091640 LEDCINE SIPPER WITH BA 1. 10.2 106 10 041051 PROLINE AND LEUCINE. 1. 10.2 857 5 018381 PAIRED BOX PROTEIN PAX 1. 10.0 290 2 051899 L-1 METALLO-BETA-LACTR 3. 10.0 833 4 099523 KIAA0634 PROTEIN (FRAG 4. 9.9 1321 4 075129 KIAA0634 PROTEIN (FRAG 4. 9.9 1321 4 075129 KIAA0634 PROTEIN (FRAG 4. 9.9 335 13 091654 HYPOTHETICAL 23.1 KD P 5. 9.7 252 2 0005192 HYPOTHETICAL 23.1 KD P 5. 9.7 252 2 0005182 HYPOTHETICAL 23.1 KD P 7.

E1 7.52e+00	SM 7.52e+00	KD P 9.83e+00	KD P 9.83e+00	OR- 9.83e+00	9.83e+00	FAC 1.28e+01	OLY 1.28e+01	FOR 1.67e+01	OR. 1.67e+01	KD P 1.67e+01	KD P 1.67e+01	KD P 1.67e+01	(F 1.67e+01	1.67e+01	H	2.17e+01	OR. 2.17e+01	T). 2.17e+01	IR ( 2.17e+01	L A 2.17e+01	N A 2.17e+01	2.17e+01	HAI 2.82e+01	PR 2.82e+01
DNA BINDING PROTEIN	SIMILARITY TO MOUSE	HYPOTHETICAL 34.4 K	HYPOTHETICAL 48.1 K	LEUCINE-RICH RECEPTOR	NB-2.	PORCINE MEMBRANE COFAC	RNA-DEPENDENT RNA POLY	ANION EXCHANGER ISOFOR	108 PROTEIN PRECURSOR	HYPOTHETICAL 30.9 K	HYPOTHETICAL 33.3 K	HYPOTHETICAL 72.6 K	ANION EXCHANGER 2 A	R32184_2.	DIACYLGLYCEROL KINASE	3' ORF.	NEUROVIRULENCE FACTOR	MYOMODULIN (FRAGMENT	MYOMODULIN PRECURSOR	LECITHIN: CHOLESTEROL	MALTASE-LIKE PROTEIN	PCBR.	MHC CLASS I HEAVY CHAI	VERY LARGE TEGUMENT
090491	018780	085011	P72841	082432	P97527	002839	083101	260471	043495	033285	069681	065568	060470	060391	000542	061639	012396	027916	007974	035849	017021	P72405	046723	P89459
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583	1238	335	410	666	1099	363	878	84	102	277	296	701	729	901	1117	147	248	329	370	440	498	551	147	3122
9.7	7.6	9.6		٠	9.6	9.5	9.5	ъ. Э.	e. ه.	9.3	ь. 9	9.3	9 .3	6.9	9.3	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1
87	87	98	86	98	98	82	82	84	84	84	84	84	84	84	84	83	83	83	83	83	83	83	82	83
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

	OI-JUN-1998 (TREMBLREL. 06, CREATED) 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) HYPOCRETIN (PREPRO-OREXIN).	HCKI. MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	ELSEQUENCE FROM N.A. MEDLINE; 98150861. SANCHAI T., CHEMELLI R.M., SANCHAI T., AMEMIYA A., ISHII M., MATSUZAKI I., CHEMELLI R.M., TARAKA H., WILLIAMS S.C., RICHARDSON J.A., KOZLOWSKI G.P., WILSON S., ARCH J.R.S., BUCKINGHAM R.E., HAYNES A.C., CARR S.A., ANNAN R.S., MOWNLITY D.E., LIU WS., TERRETI J.A., ELSHOURBAGY N.A., BERGSMA D.J. SANAGISAMA M BLING WS., TERRETI J.A., ELSHOURBAGY N.A., BERGSMA D.J.	"Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior."; CELL 92:573-585(1998).	SEQUENCE FROM N.A. SEDURALE 5804872. STRAIN-C57BL/6J; MEDLINE; 98081872. MEDLINE; 98081872. DANIELSON P.E., FUKUHARA C., BATTENBERG E.L.F., GAUTVIK V.T., BARPLETT F.S. III, FRANKEL F.S., VAN DEN POL A.N., BLOOM F.E., BARPLETT F.S. III, FRANKEL F.S., VAN DEN POL A.N., BLOOM F.E., GAUTVIK K.M., SUTCLIFFE J.G.; "The hypocretins: hypothalamus-specific peptides with neuroexcitatory activity."; PROC. NATL. ACAD. SCI. U.S.A. 95:322-327(1998). SEQUENCE FROM N.A. STRAIN-E57BL/6J; DANIELSON P.E., KILDUFF T.S., PEYRON C., GAO XB., FOYE P.E., DANIELSON P.E., FUKUHARA C., BATTENBERG E.L.F., GAUTVIK V.T., BARPLETT F.S. III, FRANKEL F.S., VAN DEN POL A.N., BLOOM F.E., SURMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF041242; G2895196; EMBL; AF019566; G2895196;
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MEDLER E., WAMBUT I., BENT E., LOVE K., GOODMAN H., DEAN C.,

MEDLER E., WAMBUT E., PATEL K., MURCHY G., PIFFANELLI P., WEDLER H.,

MEDLER E., WAMBUTT R., WEITZENEGGER T., POUL T.M., TERRYN N.,

A GIELEN J., VILLARROEL R., DE CLERCK R., VAN MONTAGU M., LECHARNY A.,

BY ANDORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,

BY ANDORG S., GY I., KREIS M., FONS A., PUGGOMENECH P., DOUKA A.,

SILVEY M., JAMES R., MONTFORT A., PONS A., PUGGOMENCH P., DOUKA A.,

HILBERT H., DUESTERHOFT A., MORGES T., JONES J.D.G., EMPYA T.,

HILBERT H., DUESTERHOFT A., MORGES W., COOKE R., BERGER C.,

A HILBERT H., VOET M., VOLCKAERI G., MEWES H.W., KLOSTERMAN S.,

A DELSENY M., VOET M., VOLCKAERI G., MEWES H.W., KLOSTERMAN S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERIEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL 74.6 KD PROTEIN.
ARABIDDPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTLES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                    68 KRRPGPPGLQGRLQRLLQASGNHAAGILTMGRRAGAEPAPRLCPGRRCLAAAASSVAPGG 127
                                                                 67
  Gaps
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                                          VSWATVTLLLLLLLLPPAVLSPGAAAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L., POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; PROC. NATL. ACAD. SCI. US.A. 0:0-0(1998).
EMBL, AF051767; G2961532; -. SEQUENCE 400 AA: 44538 MW; 6DFB5381 CRC32;
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    Indels
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EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL. 07, LAST SEQUENCE UPDATE) (TREMBLREL. 07, LAST ANNOTATION UPDATE) RECEPTOR ALPHA 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
  Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.75e-03;
atches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PWAAVTLLLLLLLPPALLSLGVDAQPLPDCCRQKTCSC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PLPPVVLMLLLLLPPSPLPLAA-GDPLPTESRLMN-SC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 AA.
                                                                                                                                                                                                                                                                                                                                                     400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.6%; Score 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 47.4%; Pred. No. Matches 18; Conservative 9; Misma
                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL. 07, CREATED)
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
13;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                     128 RSGI 131
                                                                                                                                                                                                                                                             120 GSGV 123
                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (
01-AUG-1998 (
01-AUG-1998 (
GDNF FAMILY F
66;
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060609
060609;
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023352
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "TWO homologs of the Drosophila polarity gene frizzled (fz) are widely expressed in mammalian tissues.";
J. BIOL. CHEM. 267:25207 (1992).

- FUNCTION: MAY BE INVOLVED IN TRANSDUCTION AND INTERCELLULAR TRANSMISSION OF POLARITY INFORMATION DURING TISSUE MORPHOGENESIS AND/OR IN DIFFERENTIARED TISSUES.

- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, LIVER, UTERUS, OVARY AND HEART. LOWER LEVELS SEEN IN BRAIN AND INTESTINE.

EXTREMELY LOW IN CALVARIA, MAMMARY GLANDS AND TESTIS.

- ILOWER LEVELS IN ADULT.
                                                                                                                                                                                                                                                                              598 KYCRSK-YETIHGONHDNAADVLELAIKREMPAELL-R-ASLRHTNEDQRNFLLNVGRSA 654
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=OSTEOSARCOMA;
MEDLINE; 93094228.
CHAN S.D.H., KARPF D.B., FOWLKES M.E., HOOKS M., BRADLEY M.S.,
VUONG V., BAMBINO T., LIU M.Y.C., ARNAUD C.D., STREWLER G.J.,
NISSENSON R.A.;
                                                                                                                                                                                                                                      4;
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SCHUELLER C., CHALWATZIS N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4
Arabidopsis thaliana";
NATURE 391:485-488(1998).
                                                                                                                                                                                      Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 98; DB 11; Length 641;
Pred. No. 3.44e-01;
2; Mismatches 6; Indels
                                                                                                                                                                                    Score 106; DB 10; Length 67:
Pred. No. 3.22e-02;
16; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
L; L02529; G31011; -.
ELOPMENTAL PROTEIN; TRANSMEMBRANE; GLYCOPROTEIN.
72 312 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                            B301B713 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAAVILLILLILPPALLSLGVDAQP 27
                                                                                                                                         679 AA; 74635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71027 MW;
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64.0%;
                                                                                                                                                                                    Query Match 11.8%;
Best Local Similarity 32.3%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 64.0%, nes 16; Conservative
                                                                                       EMBL; Z97337; E326841; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 AA;
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EUKARYOTA; METAZOA
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SIGNAL.
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LARVAL, ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN
LARRAL STHAT OF THE LARVAL ISOFORM.

C. -1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.

C. -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.

REMBL; X79492; E354266; --

REMBL; X79492; E354266; --

REMBL; X79492; E354266; --

REMBL; X79492; E354286; --

REMBL; X1949286; 
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                     01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
01-NOT-1998 (TREMBLEEL. 07, LAST ANNOTATION UPDATE)
PROLING- AND LEUCINE-RICH PROTEIN.
PISUM SATIVUM (GARDEN PEA).
PUKARYOTA, VIRIDIPLANIME, STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA, MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
PABALES; FABACEAE; PAPTILIONCIDEAE; PISUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERINE; 94323757.

MEDLINE; 94323757.

MEDLINE; 94323757.

MEDLINE; 94323757.

MILLDORE U., KLOTER U., GEHRING W.J.;

"Homology of the eyeless gene of Drosophila to the Small eye gene in mice and Anitidia in humans.";

SCIENCE 265:789-1789 (1994).

-I-FUNCTION: INVOLVED IN EYE MORPHOGENESIS.

-I-TISSUE SPECIFICITY: EXPRESSION IS CONFINED TO THE EYE IMAGINAL DISCS, PARTS OF THE BRAIN, THE VENTRAL GANGLION AND THE SALIVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; ARTHROPODA; TRÁCHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92; DB 10; Length lub
Pred. No. 1.90e+00;
'**ematches 4; Indels
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Pred. No. 1.90e+00;
19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                     TISSUE-PERICARP;
RODRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELTRAN J.;
SUBMITIED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 267873; E208986; -
SEQUENCE 106 Aa; 11828 MW; A45AD924 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PRELIMINARY; PRT; 857 AA. 018381 01.3781; 01.074.1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE) 01.JAN-1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE) 01.JAN-1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE)
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01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAIRED BOX PROTEIN PAX-6 (EY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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ilarity 28.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 ILLLLLLPPPLLLLLMRPLPL
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Best Local Similarity
Matches 15; Conser
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DNA_BIND
SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LLDGGMPQMAGHLLDNMKLRGVAPQDLRLILLSHAHADHAGPVAELKRRTGAHVAANA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97166212.
PETERSEN C.M., NIELSEN M.S., NYKJAER A., JACOBSEN L., TOMMERUP N., RASHUSSEN H.H., ROLGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K.; "MOLECULAR identification of a novel candidate sorting receptor purified from human brain by receptor-associated protein affinity
700 PPPMAPAHHHIVPGDGGRPAGV-GLGSGQSANLGA-SCSGSGYEVLSAYALPP 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                      STENOTROPHOMONAS MALTOPHILIA.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; LYSOBACTERALES;
XANTHOMONAS GROUP; STENOTROPHOMONAS.
                      Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 33 POTENTIAL.
34 290 L-1 METALLO-BETA-LACTAMASE.
290 AA; 30806 MW; 9B37947D CRC32;
                                                                                                                                                                                                                                                                                                                             STRAIN=GN12873;
SANGCHAGRIN F., DUFRESNE J., LEVESQUE R.C.;
SAUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF010282; G2723332;
                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 90; DB 2; Ler
Pred. No. 3.32e+00;
18; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90; DB 4; Lv
Pred. No. 3.32e+00;
5; Mismatches 6
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D2E351B9 CRC32;
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J. BIOL. CHEM. 272:3599-3605(1997).
EMBL; X98248; E246784; -.
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Search completed: Fri Aug 20 21:18:03 1999

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:10:43 1999; MasPar time 4.50 Seconds 249.097 Million cell updates/sec

Run on:

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQANGNHAAGILIM 28

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Post-processing:

122810 seqs, 40068593 residues

Searched:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 30.698; Variance 52.943; scale 0.580 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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ID	T00987	B41654	A41654	T02269	S47044	H64888	T00730	S23647	E69913	S11712	S41307	JN0443	JN0445	A55152	D69081	S49183	S19248	T02644	A33988	G01880	S25618	PRHU3	S51155
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B41654 #type complete superoxide dismutase (BC 1.15.1.1) (Cu-Zn) precursor - Haemophilus parainfluenzae formal\_name Haemophilus parainfluenzae 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 05-Mar-1999 B41654 A41654 Kroll, J.S.; Langford, P.R.; Loynds, B.M. J. Bacteriol. (1991) 173:7449-7457

ACCESSIONS REFERENCE #authors #journal

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#submission #description			o the	e EMBL Data Libra liana chromosome	Library, April 1998 some II BAC T9J22 genomic	
#accession ##status		sequence. 0987 preliminary;	inar	y; translated	from GB/EMBL/DDE	
##molecule ##residues ##cross-re	ule_type D ues 1 -reference	4 - 2	45 ##label EMBL: AC002	bel Rou 002505: NTD:	82739359: DID.02739379	
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#introns #note SUMMARY	4199,	1/1; 49/3; T9J22.21 #length 145	/8/2; #mole	8/z; 123/z #molecular-weight	ght 15355 #checksum 3045	
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                                                                                                                                                   Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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hypothetical protein F22013.25 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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#length 879 #molecular-weight 96834 #checksum 5911
           H64888 #type complete
membrane protein ydbH - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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#length 1015 #molecular-weight 111751 #checksum 6299
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#title The complete genome sequence of Escherichia col1 K-12
#cross-references MUID:97426617
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Pred. No. 5.02e+00;
6; Mismatches 6;
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brounilet, S.;
Bruschi, C.V.; Caldard, J.J.; Connerton, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizof, F.; Devine, K.M.; Duestenhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Gusseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Dev, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maucel, C.; Medique, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presecan, E.; Puinelle, D.; Porwolik, S.; Prescott,
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A.M.; Presecan, E.; Puilo, P.; Purnelle, B.; Rapport, G.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scallon, E.;
Schoeke, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Takeuchi, M.; Tanaka, T.;
Tarkemaru, K.; Takeuchi, M.; Temakoshi, A.; Tanaka, T.;
Tarkemaru, R.; Takeuchi, M.; Vanamaru, A.; Tanaka, T.;
Tarkenter, P.; Vanamaru, A.; Vanamaru, A.; Tarkeuchi, A.; Tostor, P.; Wenler, M.; Vanamaru, A.; Tarkeuchi, A.; Vanamaru, A.; Tarkeuchi, A.; Vanaman, V.; Tarkeuchi, A.; Vanaman, V.; 
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Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
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J. Cell Biol. (1992) 116:1303-1317
NuMA: an unusually long coiled-coil related protein in the
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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19-Peb-1994 #sequence_revision 10-Nov-1995 #text_change
10-Sep-1997
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Pred. No. 5.02e+00;
   S23647 #type complete
NuMA protein - human
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##residues 1-2115 ##label YAN
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Search completed: Fri Aug 20 21:10:58 1999 Job time : 15 secs.
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PAS1 protein - yeast (Pichia pastoris)
#formal_name Pichia pastoris
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                                                                                                 #domain transcription initiation factor sigma katF
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#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
17-Mar-1999
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J. Cell Biol. (1994) 127:1259-1273
Role of the PASI gene of Pichia pastoris in peroxisome
                                                                                                                                                homology #label KTF
#length 525 #molecular-weight 57204 #checksum 9676
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#length 528 #molecular-weight 57598 #checksum 7360
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Pred. No. 7.06e+00;
9; Mismatches 5; Indels
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##residues 1-528 ##label KOR
##cross-references GB:M90412; NID:g153308; PID:g153309
##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:g153305; PID:g153306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kormanec, J.; Farkasovsky, M.; Poutuckova,
Gene (1992) 122:63-70
                                                                                                                                                                                            Score 67; DB 2; LA
Pred. No. 7.06e+00;
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                                                                #superfamily Streptomyces
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#accession A55152
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Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.; Lumm, W.; Pothler, B.; Qlu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso, A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Safer, G.; Goyal, A.; Pietrokovski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, ##cross-references GB:AE000920; GB:AE000666; NID:g2622729; PID:g2622730 ##experimental\_source strain Delta H D69081 #type complete
deoxyuridine 5-triphosphate nucleotidohydrolase related
protein - Methanobacterium thermoautotrophicum (strain
Delta H) Gaps Gaps #formal\_name Methanobacterium thermoautotrophicum 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Jun-1998 #checksum 2540 #superfamily FtsH/SEC18/CDC48-type ATP-binding domain homology ATP; P-loop; peroxisome biogenesis #region nucleotide-binding motif A (P-loop)\
#domain FtsH/SEC18/CDC48-type ATP-binding domain
homology #label VATP\
#region nucleotide-binding motif A (P-loop)
#length 1157 #molecular-weight 126983 #checksum 254C J. Bacteriol. (1997) 179:7135-7155 Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis ö ·; preliminary; nucleic acid sequence not shown #length 150 #molecular-weight 16996 #checksum Score 67; DB 2; Length 1157; Pred. No. 7.06e+00; 4; Mismatches 2; Indels PID:9537420 Length 150; 4; Indels Score 66; DB 2; Le Pred. No. 9.90e+00; 5; Mismatches 4 ##Teelidues 1-1157 ##label HEY ##cross-references EMBL:236987; NID:9537419; translation not shown comparative genomics. 1-150 ##label MTH #cross-references MUID:98037514 #accession D69081 J.; Reeve, J.N. Query Match 33.3%; Best Local Similarity 60.0%; Matches 9; Conservative Query Match 32.8%; Best Local Similarity 50.0%; Matches 9; Conservative 102 GDPGFRGTLQFLLHNHGE 119

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